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METHODS FOR EVALUATING OLIGONUCLEOTIDE PROBE SEQUENCES

Appendix

This patent application includes an appendix (the "Appendix"), which contains the source code for the software used in carrying out the examples in accordance with the present invention.

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BACKGROUND OF THE INVENTION

1. Field of the Invention.

Significant morbidity and mortality are associated with infectious diseases and genetically inherited disorders. More rapid and accurate diagnostic methods are required for better monitoring and treatment of these conditions. Molecular methods using DNA probes, nucleic acid hybridization and *in vitro* amplification techniques are promising methods offering advantages to conventional methods used for patient diagnoses.

Nucleic acid hybridization has been employed for investigating the identity and establishing the presence of nucleic acids. Hybridization is based on

complementary base pairing. When complementary single stranded nucleic acids are incubated together, the complementary base sequences pair to form double-stranded hybrid molecules. The ability of single stranded deoxyribonucleic acid (ssDNA) or ribonucleic acid (RNA) to form a hydrogen bonded structure with a complementary nucleic acid sequence has been employed as an analytical tool in molecular biology research. The availability of radioactive nucleoside triphosphates of high specific activity and the development of methods for their incorporation into DNA and RNA has made it possible to identify, isolate, and characterize various nucleic acid sequences of biological interest. Nucleic acid hybridization has great potential in diagnosing disease states associated with unique nucleic acid sequences. These unique nucleic acid sequences may result from genetic or environmental change in DNA by insertions, deletions, point mutations, or by acquiring foreign DNA or RNA by means of infection by bacteria, molds, fungi, and viruses. The application of nucleic acid hybridization as a diagnostic tool in clinical medicine is limited due to the cost and effort associated with the development of sufficiently sensitive and specific methods for detecting potentially low concentrations of disease-related DNA or RNA present in the complex mixture of nucleic acid sequences found in patient samples.

One method for detecting specific nucleic acid sequences generally involves immobilization of the target nucleic acid on a solid support such as nitrocellulose paper, cellulose paper, diazotized paper, or a nylon membrane. After the target nucleic acid is fixed on the support, the support is contacted with a suitably labeled probe nucleic acid for about two to forty-eight hours. After the above time period, the solid support is washed several times at a controlled temperature to remove unhybridized probe. The support is then dried and the hybridized material is detected by autoradiography or by spectrometric methods. When very low concentrations must be detected, the above method is slow and labor intensive, and nonisotopic labels that are less readily detected than radiolabels are frequently not suitable.

A method for the enzymatic amplification of specific segments of DNA known as the polymerase chain reaction (PCR) method has been described. This *in vitro* amplification procedure is based on repeated cycles of denaturation, oligonucleotide primer annealing, and primer extension by thermophilic

polymerase, resulting in the exponential increase in copies of the region flanked by the primers. The PCR primers, which anneal to opposite strands of the DNA, are positioned so that the polymerase catalyzed extension product of one primer can serve as a template strand for the other, leading to the accumulation of a discrete fragment whose length is defined by the distance between the 5' ends of the oligonucleotide primers.

Other methods for amplifying nucleic acids have also been developed. These methods include single primer amplification, ligase chain reaction (LCR), transcription-mediated amplification methods including 3SR and NASBA, and the Q-beta-replicase method. Regardless of the amplification used, the amplified product must be detected.

One method for detecting nucleic acids is to employ nucleic acid probes that have sequences complementary to sequences in the target nucleic acid. A nucleic acid probe may be, or may be capable of being, labeled with a reporter group or may be, or may be capable of becoming, bound to a support. Detection of signal depends upon the nature of the label or reporter group. Usually, the probe is comprised of natural nucleotides such as ribonucleotides and deoxyribonucleotides and their derivatives although unnatural nucleotide mimetics such as peptide nucleic acids and oligomeric nucleoside phosphonates are also used. Commonly, binding of the probes to the target is detected by means of a label incorporated into the probe. Alternatively, the probe may be unlabeled and the target nucleic acid labeled. Binding can be detected by separating the bound probe or target from the free probe or target and detecting the label. In one approach, a sandwich is formed comprised of one probe, which may be labeled, the target and a probe that is or can become bound to a surface. Alternatively, binding can be detected by a change in the signal-producing properties of the label upon binding, such as a change in the emission efficiency of a fluorescent or chemiluminescent label. This permits detection to be carried out without a separation step. Finally, binding can be detected by labeling the target, allowing the target to hybridize to a surface-bound probe, washing away the unbound target and detecting the labeled target that remains.

Direct detection of labeled target hybridized to surface-bound probes is particularly advantageous if the surface contains a mosaic of different probes that

are individually localized to discrete, known areas of the surface. Such ordered arrays containing a large number of oligonucleotide probes have been developed as tools for high throughput analyses of genotype and gene expression.

Oligonucleotides synthesized on a solid support recognize uniquely

5 complementary nucleic acids by hybridization, and arrays can be designed to define specific target sequences, analyze gene expression patterns or identify specific allelic variations. One difficulty in the design of oligonucleotide arrays is that oligonucleotides targeted to different regions of the same gene can show large differences in hybridization efficiency, presumably due, at least in part, to
10 the interplay between the secondary structures of the oligonucleotides and their targets and the stability of the final probe/target hybridization product. A method for predicting which oligonucleotides will show detectable hybridization would substantially decrease the number of iterations required for optimal array design and would be particularly useful when the total number of oligonucleotide probes
15 on the array is limited. A method to predict oligonucleotide hybridization efficiency would also streamline the empirical approaches currently used to select potential antisense therapeutics, which are designed to modulate gene expression *in vivo* by hybridizing to specific messenger RNA (mRNA) molecules and inhibiting their translation into proteins.

20 While it is well known that the structure of the target nucleic acid affects the affinity of oligonucleotide hybridization, current methods for predicting target structures from the primary sequence fail to predict target regions accessible for oligonucleotide binding. Consequently, selection of oligonucleotides for antisense reagents or oligonucleotide probe arrays has been largely empirical. As most of
25 the target sequence is sequestered by intramolecular base pairing and not accessible for oligonucleotide binding, the process of identifying good oligonucleotides has required large numbers of low efficiency experiments.

The design and implementation of algorithms that effectively predict the ability of oligonucleotides to rapidly and avidly bind to complementary nucleotide
30 sequences has been an important problem in molecular biology since the invention of facile methods for chemical DNA synthesis. The subsequent inventions of the polymerase chain reaction (PCR), antisense inhibition of gene expression and oligonucleotide array methods for performing massively parallel

hybridization experiments have made the need for effective predictive algorithms even more critical.

Previous attempts to solve the nucleic acid probe design problem include PCR primer design software applications (e.g., OLIGO®), neural networks, PCR primer design applications that search for sequences that possess minimal ability to cross-hybridize with other targets present in a sample (e.g., HYBsimulator™), and approaches that attempt to predict the efficiency of antisense sequence suppression of mRNA translation from a combination of predicted nucleic acid duplex melting temperature and predicted target strand structure. The methods that predict effective oligonucleotide primers for performing PCR from DNA templates work well for that application where relatively stringent conditions are employed. This is because PCR experimental design greatly simplifies the prediction problem: hybridization is performed at high temperature, at relatively low ionic strength and in the presence of a large molar excess of oligonucleotide. Under these conditions, the oligonucleotide and target secondary structures are relatively unimportant.

Unfortunately, these conditions do not apply to oligonucleotide arrays, which are usually hybridized under relatively non-denaturing conditions, or to antisense suppression of gene expression, which takes place *in vivo*. Oligonucleotide arrays can contain hundreds of thousands of different sequences and conditions are chosen to allow the oligonucleotide with the lowest melting temperature to hybridize efficiently. These "lowest common denominator" conditions are usually relatively non-denaturing and secondary structure constraints become significant. Accordingly, the above applications require new predictive methods that are capable of estimating the effects of oligonucleotide and target structure on hybridization efficiency. For these reasons, current algorithms for designing PCR primer oligonucleotides fail badly when applied to the problems of oligonucleotide array or antisense oligonucleotide design.

To date, the most effective approach for identifying oligonucleotides with good hybridization efficiency has been an empirical one. Such an approach involves the synthesis of large numbers of oligonucleotide probes for a given target nucleotide sequence. Arrays are formed that include the above oligonucleotide probes. Hybridization experiments are carried out to determine

which of the oligonucleotide probes exhibit good hybridization efficiencies. Examples of such an approach are found in D. Lockhart, et al., Nature Biotech., *infra*, L. Wodicka, et al., Nature Biotechnology, *infra.*, and N. Milner et al. Nature Biotech, *infra*. One major drawback to this approach is the vast number of
5 oligonucleotides that must be synthesized in order to achieve a satisfactory result. Typically, about 2%-5% of the test probes synthesized yield acceptable signal levels.

The use of neural networks for oligonucleotide design has also been investigated. Neural networks are easily taught with real data; they therefore
10 afford a general approach to many problems. However, their performance is limited by the "senses" that they are given. An analogy works best here: the human brain is an astoundingly capable neural network, but a blind person cannot be taught to reliably distinguish colors by smell. In addition, a large amount of data is required to adequately teach a neural network to perform its job well. A
15 comprehensive database for either oligonucleotide array design or antisense suppression of gene expression has not been made available. For these reasons, the performance reported to-date of neural network solutions against the probe design problem is mediocre.

Finally, approaches that have attempted to use target nucleic acid folding
20 calculations to predict experimental results inferred to depend upon hybridization efficiency (e.g. antisense suppression of mRNA translation) have so far only demonstrated that the predictions of current nucleic acid folding calculations correlate poorly with observed behavior. The probable reason for this is that the structures predicted by such programs for long sequences are poor predictors of
25 chemical reality; the results of experiments that attempt to confirm the predictions of such calculations support this assessment. Recent improvements to this approach which use predicted RNA structure topology as a predictor of relative RNA/RNA association kinetics have been more successful at forecasting the results of antisense experiments. However, these methods are not
30 computationally efficient, and have so far only been shown to work for targets less than 100 bases long. Such methods are therefore not yet capable of predicting the behavior of full-length mRNA targets, which are typically between 1,000 and 2,000 bases in length.

2. Description of the Related Art.

U.S. Patent No. 5,512,438 (Ecker) discloses the inhibition of RNA expression by forming a pseudo-half knot RNA at the target's RNA secondary structure using antisense oligonucleotides.

Cook, *et al.*, in U.S. Patent No. 5,670,633 discuss sugar-modified oligonucleotides that detect and modulate gene expression.

Antisense oligonucleotide inhibition of the RAS gene is disclosed in U.S. Patent No. 5,582,986 (Monia, *et al.*).

U.S. Patent No. 5,593,834 (Lane, *et al.*) discusses a method of preparing DNA sequences with known ligand binding characteristics.

Mitsuhashi, *et al.*, in U.S. Patent No. 5,556,749 discusses a computerized method for designing optimal DNA probes and an oligonucleotide probe design station.

U.S. Patent No. 5,081,584 (Omichinski, *et al.*) discloses a computer-assisted design of anti-peptides based on the amino acid sequence of a target peptide.

A PCR primer design application that searches for sequences that possess minimal ability to cross-hybridize with other targets present in a sample is available as HYBsimulator™, version 2.0, AGCT, Inc., 2102 Business Center Drive, Suite 170, Irvine, CA 92715 (714) 833-9983.

A PCR primer design software application is available as OLIGO®, version 5.0, National Biosciences, Inc., 3650 Annapolis Lane North, #140, Plymouth, MN 55447 (800) 747-4362.

D. J. Lockhart, *et al.*, Nature Biotech. 14:1675-1684 (1996) describe a neural network approach to the selection of efficient surface-bound oligonucleotide probes.

M. Mitsuhashi, *et al.*, Nature, 367:759-761 (1994) disclose a method for designing specific oligonucleotide probes and primers by modeling the potential cross-hybridization of candidate probes to non-target sequences known to be present in samples.

R. A. Stull, *et al.*, Nuc. Acids Res., 20:3501-3508 (1992) describe a method of predicting the efficacy of antisense oligonucleotides, using predicted target

secondary structure and predicted oligonucleotide/target binding free energy as input parameters.

N. Milner, *et al.*, Nature Biotechnology, 15:537-541 (1997) compare observed patterns of probe hybridization to those expected from the predicted
5 secondary structure of the nucleic acid target.

L. Wodicka, *et al.*, Nature Biotechnology, 15:1359-1367 (1997) describe simple rules for avoiding inefficient and non-specific probes during design and synthesis of oligonucleotides arrays.

J. SantaLucia Jr., *et al.*, Biochemistry, 35:3555 (1996) disclose parameters
10 and methods for the calculation of thermodynamic properties of DNA/DNA homoduplexes.

N. Sugimoto, *et al.*, Biochemistry, 34:11211 (1995) disclose parameters and methods for the calculation of thermodynamic properties of DNA/RNA heteroduplexes.

J.A. Jaeger, *et al.*, Proc. Natl. Acad. Sci. USA, 86:7706 (1989) disclose
15 methods for estimation of the free energy of the most stable intramolecular structure of a single-stranded polynucleotide, by means of a dynamic programming algorithm.

S. F. Altschul, *et al.*, Nature Genetics, 6:119-129 (1994) disclose methods
20 for calculating the complexity and information content of amino acid and nucleic acid sequences.

T. A. Weber and E. Helfand, J. Chem. Phys., 71, 4760 (1979) describe approaches for the modeling of polymer structures by molecular dynamics simulations.

V. Patzel and G. Sczakiel, Nature Biotech., 16, 64-68 (1998) disclose
25 methods for estimating rate constants for association of antisense RNA molecules with mRNA targets by examination of predicted antisense RNA secondary structures.

Light-generated oligonucleotide arrays for rapid DNA sequence analysis is
30 described by A. C. Pease, *et al.*, Proc. Nat. Acad. Sci. USA (1994) 91:5022-5026.

Mitsuhashi discusses basic requirements for designing optimal oligonucleotide probe sequences in J. Clinical Laboratory Analysis (1996) 10:277-284.

Rychlik, *et al.*, discloses a computer program for choosing optimal oligonucleotides for filter hybridization, sequencing and in vitro amplification of DNA in Nucleic Acids Research (1989) 17(21):8543-8551.

5 A strategy for designing specific antisense oligonucleotide sequences is described by Mitsuhashi in J. Gastroenterol. (1997) 32:282-287.

Mitsuhashi discusses basic requirements for designing optimal PCR primers in J. Clinical Laboratory Analysis (1996) 10:285-293.

10 Hyndman, *et al.*, disclose software to determine optimal oligonucleotide sequences based on hybridization simulation data in BioTechniques (1996) 20(6):1090-1094.

Eberhardt discloses a shell program for the design of PCR primers using genetics computer group (GCG) software (7.1) on VAX/VMS™ systems in BioTechniques (1992) 13(6):914-917.

15 Chen, *et al.*, disclose a computer program for calculating the melting temperature of degenerate oligonucleotides used in PCR or hybridization in BioTechniques (1997) 22(6):1158-1160.

20 Partial thermodynamic parameters for prediction stability and washing behavior of DNA duplexes immobilized on gel matrix is described by Kunitsyn, *et al.*, in J. Biomolecular Structure & Dynamics, ISSN 0739-1102 (1996) 14(1):239-244.

SUMMARY OF THE INVENTION

One embodiment of the present invention is a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A
25 predetermined set of unique oligonucleotide sequences is identified. The unique oligonucleotide sequences are chosen to sample the entire length of a nucleotide sequence that is hybridizable with the target nucleotide sequence. At least one parameter that is predictive of the ability of each of the oligonucleotides specified by the set of sequences to hybridize to the target nucleotide sequence is
30 determined and evaluated for each of the above oligonucleotide sequences. A subset of oligonucleotide sequences within the predetermined set of unique oligonucleotide sequences is identified based on the examination of the parameter values. Finally, oligonucleotide sequences in the subset are identified that are

clustered along one or more regions of the nucleotide sequence that is hybridizable to the target nucleotide sequence. The oligonucleotide probes corresponding to the identified sequences find use in polynucleotide assays particularly where the assays involve oligonucleotide arrays. For a discussion of
5 oligonucleotide arrays, see, e.g., U.S. Patent No. 5,700,637 (E. Southern) and U.S. Patent No. 5,667,667 (E. Southern), the relevant disclosures of which are incorporated herein by reference.

Another embodiment of the present invention is a method for predicting the potential of an oligonucleotide to hybridize to a complementary target nucleotide
10 sequence. A set of overlapping oligonucleotide sequences is identified based on a nucleotide sequence that is complementary to the target nucleotide sequence. At least two parameters that are independently predictive of the ability of each of the oligonucleotides specified by the oligonucleotide sequences to hybridize to the target nucleotide sequence are determined and evaluated for each of the
15 oligonucleotide sequences. Independence is assured by requiring that the parameters be poorly correlated with respect to one another. A subset of oligonucleotide sequences within the set of oligonucleotide sequences is identified based on the examination of the parameter values. Finally, oligonucleotide sequences in the subset are identified that are clustered along one or more
20 regions of the nucleotide sequence that is complementary to the target nucleotide sequence.

Another embodiment of the present invention is a method for predicting the potential of an oligonucleotide to hybridize to a complementary target nucleotide sequence. A set of overlapping oligonucleotide sequences is obtained based on a
25 nucleotide sequence of length L, complementary to the target nucleotide sequence. The oligonucleotide sequences of the set of overlapping oligonucleotide sequences are of identical length N and spaced one nucleotide apart. The set comprises L-N+1 oligonucleotide sequences. Parameters are determined for each of the oligonucleotide sequences of the set of overlapping
30 oligonucleotide sequences. One parameter is the predicted melting temperature of the duplex of each of the oligonucleotides specified by the oligonucleotide sequences and the target nucleotide sequence, corrected for salt concentration. The other parameter is the predicted free energy of the most stable intramolecular

structure of each of the oligonucleotides specified by the oligonucleotide sequences at the temperature of hybridization of the oligonucleotide with the target nucleotide sequence. A subset of oligonucleotide sequences within the set of oligonucleotide sequences is selected based on an examination of the parameter values by establishing cut-off values for each of the parameters. Oligonucleotide sequences in the subset that are clustered along one or more regions of the complementary nucleotide sequence are ranked based on the sizes of the clusters of oligonucleotide sequences. Finally, a subset of the clustered oligonucleotide sequences is selected that statistically samples the clusters of oligonucleotide sequences. The selected sampled subset is used to specify the synthesis of oligonucleotides for experimental evaluation.

Another aspect of the present invention is a computer based method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides within a nucleotide sequence that is hybridizable with the target nucleotide sequence is identified under computer control. The oligonucleotides are chosen to sample the entire length of the nucleotide sequence. A value is determined and evaluated under computer control for each of the oligonucleotides for at least one parameter that is independently predictive of the ability of each of the oligonucleotides to hybridize to the target nucleotide sequence. The parameter values are stored. A subset of oligonucleotides within the predetermined number of unique oligonucleotides is identified by examination of the stored parameter values under computer control. Then, oligonucleotides in the subset that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence are identified under computer control.

Another aspect of the present invention is a computer system for conducting a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. The system comprises (a) input means for introducing a target nucleotide sequence into the computer system, (b) means for determining a number of unique oligonucleotide sequences that are within a nucleotide sequence that is hybridizable with the target nucleotide sequence where the oligonucleotide sequences are chosen to sample the entire length of the nucleotide sequence, (c) memory means for storing the oligonucleotide

sequences, (d) means for controlling the computer system to carry out for each of the oligonucleotide sequences a determination and evaluation of a value for at least one parameter that is independently predictive of the ability of each of the oligonucleotide sequences to hybridize to the target nucleotide sequence, (e) means for storing the parameter values, (f) means for controlling the computer to carry out an identification from the stored parameter values a subset of oligonucleotide sequences within the number of unique oligonucleotide sequences based on the examination of the parameter, (g) means for storing the subset of oligonucleotides, (h) means for controlling the computer to carry out an identification of oligonucleotide sequences in the subset that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence, (i) means for storing the oligonucleotide sequences in the subset, and (j) means for outputting data relating to the oligonucleotide sequences in the subset.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a general flow chart depicting the method of the present invention.

Fig. 2 is a flow chart depicting a preferred embodiment of a method in accordance with the present invention.

Fig. 3 is a contour plot of normalized hybridization intensity from multiple experiments, as a function of the free energy of the most stable probe intramolecular structure (ΔG_{MFOLD}) and the difference between the predicted RNA/DNA heteroduplex melting temperature (T_m) and the temperature of hybridization (T_{hyb}).

Fig. 4 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to a portion of the rabbit β -globin gene (radiolabeled antisense RNA target).

Fig. 5 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to the HIV PRT gene (fluorescein-labeled sense RNA target).

Fig. 6 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to the G3PDH gene (fluorescein-labeled antisense RNA target).

Fig. 7 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to the p53 gene (fluorescein-labeled antisense RNA target).

Fig. 8 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to the HIV PRTs gene (using data from the GeneChip™ data).

DEFINITIONS

Before proceeding further with a description of the specific embodiments of the present invention, a number of terms will be defined.

Nucleic Acids:

Polynucleotide -- a compound or composition that is a polymeric nucleotide or nucleic acid polymer. The polynucleotide may be a natural compound or a synthetic compound. In the context of an assay, the polynucleotide is often referred to as a polynucleotide analyte. The polynucleotide can have from about 20 to 5,000,000 or more nucleotides. The larger polynucleotides are generally found in the natural state. In an isolated state the polynucleotide can have about 30 to 50,000 or more nucleotides, usually about 100 to 20,000 nucleotides, more frequently 500 to 10,000 nucleotides. It is thus obvious that isolation of a polynucleotide from the natural state often results in fragmentation. The polynucleotides include nucleic acids, and fragments thereof, from any source in purified or unpurified form including DNA (dsDNA and ssDNA) and RNA, including tRNA, mRNA, rRNA, mitochondrial DNA and RNA, chloroplast DNA and RNA, DNA/RNA hybrids, or mixtures thereof, genes, chromosomes, plasmids, the genomes of biological material such as microorganisms, e.g., bacteria, yeasts, viruses, viroids, molds, fungi, plants, animals, humans, and the like. The polynucleotide can be only a minor fraction of a complex mixture such as a biological sample. Also included are genes, such as hemoglobin gene for sickle-cell anemia, cystic fibrosis gene, oncogenes, cDNA, and the like.

The polynucleotide can be obtained from various biological materials by procedures well known in the art. The polynucleotide, where appropriate, may be cleaved to obtain a fragment that contains a target nucleotide sequence, for example, by shearing or by treatment with a restriction endonuclease or other site specific chemical cleavage method.

For purposes of this invention, the polynucleotide, or a cleaved fragment obtained from the polynucleotide, will usually be at least partially denatured or single stranded or treated to render it denatured or single stranded. Such treatments are well known in the art and include, for instance, heat or alkali treatment, or enzymatic digestion of one strand. For example, dsDNA can be heated at 90-100° C. for a period of about 1 to 10 minutes to produce denatured material.

Target nucleotide sequence -- a sequence of nucleotides to be identified, usually existing within a portion or all of a polynucleotide, usually a polynucleotide analyte. The identity of the target nucleotide sequence generally is known to an extent sufficient to allow preparation of various sequences hybridizable with the target nucleotide sequence and of oligonucleotides, such as probes and primers, and other molecules necessary for conducting methods in accordance with the present invention, an amplification of the target polynucleotide, and so forth.

The target sequence usually contains from about 30 to 5,000 or more nucleotides, preferably 50 to 1,000 nucleotides. The target nucleotide sequence is generally a fraction of a larger molecule or it may be substantially the entire molecule such as a polynucleotide as described above. The minimum number of nucleotides in the target nucleotide sequence is selected to assure that the presence of a target polynucleotide in a sample is a specific indicator of the presence of polynucleotide in a sample. The maximum number of nucleotides in the target nucleotide sequence is normally governed by several factors: the length of the polynucleotide from which it is derived, the tendency of such polynucleotide to be broken by shearing or other processes during isolation, the efficiency of any procedures required to prepare the sample for analysis (e.g. transcription of a DNA template into RNA) and the efficiency of detection and/or amplification of the target nucleotide sequence, where appropriate.

Oligonucleotide -- a polynucleotide, usually single stranded, usually a synthetic polynucleotide but may be a naturally occurring polynucleotide. The oligonucleotide(s) are usually comprised of a sequence of at least 5 nucleotides, preferably, 10 to 100 nucleotides, more preferably, 20 to 50 nucleotides, and usually 10 to 30 nucleotides, more preferably, 20 to 30 nucleotides, and desirably about 25 nucleotides in length.

Various techniques can be employed for preparing an oligonucleotide. Such oligonucleotides can be obtained by biological synthesis or by chemical synthesis. For short sequences (up to about 100 nucleotides), chemical synthesis will frequently be more economical as compared to the biological synthesis. In addition to economy, chemical synthesis provides a convenient way of incorporating low molecular weight compounds and/or modified bases during specific synthesis steps. Furthermore, chemical synthesis is very flexible in the choice of length and region of the target polynucleotide binding sequence. The oligonucleotide can be synthesized by standard methods such as those used in commercial automated nucleic acid synthesizers. Chemical synthesis of DNA on a suitably modified glass or resin can result in DNA covalently attached to the surface. This may offer advantages in washing and sample handling. For longer sequences standard replication methods employed in molecular biology can be used such as the use of M13 for single stranded DNA as described by J. Messing (1983) Methods Enzymol, 101:20-78.

Other methods of oligonucleotide synthesis include phosphotriester and phosphodiester methods (Narang, *et al.* (1979) Meth. Enzymol 68:90) and synthesis on a support (Beaucage, *et al.* (1981) Tetrahedron Letters 22:1859-1862) as well as phosphoramidite techniques (Caruthers, M. H., *et al.*, "Methods in Enzymology," Vol. 154, pp. 287-314 (1988)) and others described in "Synthesis and Applications of DNA and RNA," S.A. Narang, editor, Academic Press, New York, 1987, and the references contained therein. The chemical synthesis via a photolithographic method of spatially addressable arrays of oligonucleotides bound to glass surfaces is described by A. C. Pease, *et al.*, Proc. Nat. Acad. Sci. USA (1994) 91:5022-5026.

Oligonucleotide probe -- an oligonucleotide employed to bind to a portion of a polynucleotide such as another oligonucleotide or a target nucleotide sequence.

The design and preparation of the oligonucleotide probes are generally dependent upon the sensitivity and specificity required, the sequence of the target polynucleotide and, in certain cases, the biological significance of certain portions of the target polynucleotide sequence.

5 Oligonucleotide primer(s) -- an oligonucleotide that is usually employed in a chain extension on a polynucleotide template such as in, for example, an amplification of a nucleic acid. The oligonucleotide primer is usually a synthetic nucleotide that is single stranded, containing a sequence at its 3'-end that is capable of hybridizing with a defined sequence of the target polynucleotide.

10 Normally, an oligonucleotide primer has at least 80%, preferably 90%, more preferably 95%, most preferably 100%, complementarity to a defined sequence or primer binding site. The number of nucleotides in the hybridizable sequence of an oligonucleotide primer should be such that stringency conditions used to hybridize the oligonucleotide primer will prevent excessive random non-specific
15 hybridization. Usually, the number of nucleotides in the oligonucleotide primer will be at least as great as the defined sequence of the target polynucleotide, namely, at least ten nucleotides, preferably at least 15 nucleotides, and generally from about 10 to 200, preferably 20 to 50, nucleotides.

In general, in primer extension, amplification primers hybridize to, and are
20 extended along (chain extended), at least the target nucleotide sequence within the target polynucleotide and, thus, the target sequence acts as a template. The extended primers are chain "extension products." The target sequence usually lies between two defined sequences but need not. In general, the primers hybridize with the defined sequences or with at least a portion of such target
25 polynucleotide, usually at least a ten-nucleotide segment at the 3'-end thereof and preferably at least 15, frequently a 20 to 50 nucleotide segment thereof.

Nucleoside triphosphates -- nucleosides having a 5'-triphosphate
substituent. The nucleosides are pentose sugar derivatives of nitrogenous bases of either purine or pyrimidine derivation, covalently bonded to the 1'-carbon of the
30 pentose sugar, which is usually a deoxyribose or a ribose. The purine bases include adenine (A), guanine (G), inosine (I), and derivatives and analogs thereof. The pyrimidine bases include cytosine (C), thymine (T), uracil (U), and derivatives and analogs thereof. Nucleoside triphosphates include deoxyribonucleoside

triphosphates such as the four common deoxyribonucleoside triphosphates dATP, dCTP, dGTP and dTTP and ribonucleoside triphosphates such as the four common triphosphates rATP, rCTP, rGTP and rUTP.

The term "nucleoside triphosphates" also includes derivatives and analogs thereof, which are exemplified by those derivatives that are recognized and polymerized in a similar manner to the underivatized nucleoside triphosphates.

Nucleotide -- a base-sugar-phosphate combination that is the monomeric unit of nucleic acid polymers, i.e., DNA and RNA. The term "nucleotide" as used herein includes modified nucleotides as defined below.

DNA -- deoxyribonucleic acid.

RNA -- ribonucleic acid.

Modified nucleotide -- a unit in a nucleic acid polymer that contains a modified base, sugar or phosphate group. The modified nucleotide can be produced by a chemical modification of the nucleotide either as part of the nucleic acid polymer or prior to the incorporation of the modified nucleotide into the nucleic acid polymer. For example, the methods mentioned above for the synthesis of an oligonucleotide may be employed. In another approach a modified nucleotide can be produced by incorporating a modified nucleoside triphosphate into the polymer chain during an amplification reaction. Examples of modified nucleotides, by way of illustration and not limitation, include dideoxynucleotides, derivatives or analogs that are biotinylated, amine modified, alkylated, fluorophore-labeled, and the like and also include phosphorothioate, phosphite, ring atom modified derivatives, and so forth.

Nucleoside -- is a base-sugar combination or a nucleotide lacking a phosphate moiety.

Nucleotide polymerase -- a catalyst, usually an enzyme, for forming an extension of a polynucleotide along a DNA or RNA template where the extension is complementary thereto. The nucleotide polymerase is a template dependent polynucleotide polymerase and utilizes nucleoside triphosphates as building blocks for extending the 3'-end of a polynucleotide to provide a sequence complementary with the polynucleotide template. Usually, the catalysts are enzymes, such as DNA polymerases, for example, prokaryotic DNA polymerase (I, II, or III), T4 DNA polymerase, T7 DNA polymerase, Klenow fragment, reverse

transcriptase, Vent DNA polymerase, Pfu DNA polymerase, Taq DNA polymerase, and the like, or RNA polymerases, such as T3 and T7 RNA polymerases. Polymerase enzymes may be derived from any source such as cells, bacteria such as E. coli, plants, animals, virus, thermophilic bacteria, and so forth.

Amplification of nucleic acids or polynucleotides -- any method that results in the formation of one or more copies of a nucleic acid or polynucleotide molecule (exponential amplification) or in the formation of one or more copies of only the complement of a nucleic acid or polynucleotide molecule (linear amplification).

Hybridization (hybridizing) and binding -- in the context of nucleotide sequences these terms are used interchangeably herein. The ability of two nucleotide sequences to hybridize with each other is based on the degree of complementarity of the two nucleotide sequences, which in turn is based on the fraction of matched complementary nucleotide pairs. The more nucleotides in a given sequence that are complementary to another sequence, the more stringent the conditions can be for hybridization and the more specific will be the binding of the two sequences. Increased stringency is achieved by elevating the temperature, increasing the ratio of co-solvents, lowering the salt concentration, and the like.

Hybridization efficiency -- the productivity of a hybridization reaction, measured as either the absolute or relative yield of oligonucleotide probe/polynucleotide target duplex formed under a given set of conditions in a given amount of time.

Homologous or substantially identical polynucleotides -- In general, two polynucleotide sequences that are identical or can each hybridize to the same polynucleotide sequence are homologous. The two sequences are homologous or substantially identical where the sequences each have at least 90%, preferably 100%, of the same or analogous base sequence where thymine (T) and uracil (U) are considered the same. Thus, the ribonucleotides A, U, C and G are taken as analogous to the deoxynucleotides dA, dT, dC, and dG, respectively. Homologous sequences can both be DNA or one can be DNA and the other RNA.

Complementary -- Two sequences are complementary when the sequence of one can bind to the sequence of the other in an anti-parallel sense wherein the 3'-end of each sequence binds to the 5'-end of the other sequence and each A, T(U), G, and C of one sequence is then aligned with a T(U), A, C, and G, respectively, of the other sequence. RNA sequences can also include complementary G/U or U/G basepairs.

Member of a specific binding pair ("sbp member") -- one of two different molecules, having an area on the surface or in a cavity that specifically binds to and is thereby defined as complementary with a particular spatial and polar organization of the other molecule. The members of the specific binding pair are referred to as cognates or as ligand and receptor (antiligand). These may be members of an immunological pair such as antigen-antibody, or may be operator-repressor, nuclease-nucleotide, biotin-avidin, hormones-hormone receptors, nucleic acid duplexes, IgG-protein A, DNA-DNA, DNA-RNA, and the like.

Ligand -- any compound for which a receptor naturally exists or can be prepared.

Receptor ("antiligand") -- any compound or composition capable of recognizing a particular spatial and polar organization of a molecule, e.g., epitopic or determinant site. Illustrative receptors include naturally occurring receptors, e.g., thyroxine binding globulin, antibodies, enzymes, Fab fragments, lectins, nucleic acids, repressors, protection enzymes, protein A, complement component C1q, DNA binding proteins or ligands and the like.

Oligonucleotide Properties:

Potential of an oligonucleotide to hybridize -- the combination of duplex formation rate and duplex dissociation rate that determines the amount of duplex nucleic acid hybrid that will form under a given set of experimental conditions in a given amount of time.

Parameter -- a factor that provides information about the hybridization of an oligonucleotide with a target nucleotide sequence. Generally, the factor is one that is predictive of the ability of an oligonucleotide to hybridize with a target

nucleotide sequence. Such factors include composition factors, thermodynamic factors, chemosynthetic efficiencies, kinetic factors, and the like.

Parameter predictive of the ability to hybridize -- a parameter calculated from a set of oligonucleotide sequences wherein the parameter positively
5 correlates with observed hybridization efficiencies of those sequences. The parameter is, therefore, predictive of the ability of those sequences to hybridize. "Positive correlation" can be rigorously defined in statistical terms. The correlation coefficient $\rho_{x,y}$ of two experimentally measured discrete quantities x and y (N values in each set) is defined as

$$\rho_{x,y} = \frac{\text{Covariance}(x,y)}{\sqrt{\text{Variance}(x)\text{Variance}(y)}},$$

where the Covariance (x,y) is defined by

$$\text{Covariance}(x,y) = \frac{1}{N} \sum_{j=1}^N (x_j - \mu_x)(y_j - \mu_y).$$

The quantities μ_x and μ_y are the averages of the quantities x and y , while the variances are simply the squares of the standard deviations (defined below). The correlation coefficient is a dimensionless (unitless) quantity between -1 and 1 . A
20 correlation coefficient of 1 or -1 indicates that x and y have a linear relationship with a positive or negative slope, respectively. A correlation coefficient of zero indicates no relationship; for example, two sets of random numbers will yield a correlation coefficient near zero. Intermediate correlation coefficients indicate intermediate degrees of relatedness between two sets of numbers. The
25 correlation coefficient is a good statistical measure of the degree to which one set of numbers predicts a second set of numbers.

Composition factor -- a numerical factor based solely on the composition or sequence of an oligonucleotide without involving additional parameters, such as experimentally measured nearest-neighbor thermodynamic parameters. For
30 instance, the fraction $(G+C)$, given by the formula

$$f_{GC} = \frac{n_G + n_C}{n_G + n_C + n_A + n_{T \text{ or } U}},$$

where n_G , n_C , n_A and $n_{T \text{ or } U}$ are the numbers of G, C, A and T (or U) bases in an oligonucleotide, is an example of a composition factor. Examples of composition factors, by way of illustration and not limitation, are mole fraction (G+C), percent (G+C), sequence complexity, sequence information content, frequency of occurrence of specific oligonucleotide sequences in a sequence database and so forth.

Thermodynamic factor -- numerical factors that predict the behavior of an oligonucleotide in some process that has reached equilibrium. For instance, the free energy of duplex formation between an oligonucleotide and its complement is a thermodynamic factor. Thermodynamic factors for systems that can be subdivided into constituent parts are often estimated by summing contributions from the constituent parts. Such an approach is used to calculate the thermodynamic properties of oligonucleotides.

Examples of thermodynamic factors, by way of illustration and not limitation, are predicted duplex melting temperature, predicted enthalpy of duplex formation, predicted entropy of duplex formation, free energy of duplex formation, predicted melting temperature of the most stable intramolecular structure of the oligonucleotide or its complement, predicted enthalpy of the most stable intramolecular structure of the oligonucleotide or its complement, predicted entropy of the most stable intramolecular structure of the oligonucleotide or its complement, predicted free energy of the most stable intramolecular structure of the oligonucleotide or its complement, predicted melting temperature of the most stable hairpin structure of the oligonucleotide or its complement, predicted enthalpy of the most stable hairpin structure of the oligonucleotide or its complement, predicted entropy of the most stable hairpin structure of the oligonucleotide or its complement, predicted free energy of the most stable hairpin structure of the oligonucleotide or its complement, thermodynamic partition function for intramolecular structure of the oligonucleotide or its complement and the like.

Chemosynthetic efficiency -- oligonucleotides and nucleotide sequences may both be made by sequential polymerization of the constituent nucleotides. However, the individual addition steps are not perfect; they instead proceed with some fractional efficiency that is less than unity. This may vary as a function of position in the sequence. Therefore, what is really produced is a family of molecules that consists of the desired molecule plus many truncated sequences. These "failure sequences" affect the observed efficiency of hybridization between an oligonucleotide and its complementary target. Examples of chemosynthetic efficiency factors, by way of illustration and not limitation, are coupling efficiencies, overall efficiencies of the synthesis of a target nucleotide sequence or an oligonucleotide probe, and so forth.

Kinetic factor -- numerical factors that predict the rate at which an oligonucleotide hybridizes to its complementary sequence or the rate at which the hybridized sequence dissociates from its complement are called kinetic factors. Examples of kinetic factors are steric factors calculated via molecular modeling or measured experimentally, rate constants calculated via molecular dynamics simulations, associative rate constants, dissociative rate constants, enthalpies of activation, entropies of activation, free energies of activation, and the like.

Predicted duplex melting temperature -- the temperature at which an oligonucleotide mixed with a hybridizable nucleotide sequence is predicted to form a duplex structure (double-helix hybrid) with 50% of the hybridizable sequence. At higher temperatures, the amount of duplex is less than 50%; at lower temperatures, the amount of duplex is greater than 50%. The melting temperature T_m ($^{\circ}\text{C}$) is calculated from the enthalpy (ΔH), entropy (ΔS) and C , the concentration of the most abundant duplex component (for hybridization arrays, the soluble hybridization target), using the equation

$$T_m = \frac{\Delta H}{\Delta S + R \ln C} - 273.15,$$

where R is the gas constant, $1.987 \text{ cal}/(\text{mole} \cdot ^{\circ}\text{K})$. For longer sequences (>100 nucleotides), T_m can also be estimated from the mole fraction ($G+C$), χ_{G+C} , using the equation

$$T_m = 81.5 + 41.0 \chi_{G+C}.$$

Melting temperature corrected for salt concentration -- polynucleotide duplex melting temperatures are calculated with the assumption that the concentration of sodium ion, Na^+ , is 1 M. Melting temperatures T'_m calculated for duplexes formed at different salt concentrations are corrected via the semi-empirical equation

$$T'_m([Na^+]) = T_m + 16.6 \log([Na^+]).$$

Predicted enthalpy, entropy and free energy of duplex formation -- the enthalpy (ΔH), entropy and free energy (ΔG) are thermodynamic state functions, related by the equation

$$\Delta G = \Delta H - T \Delta S,$$

where T is the temperature in $^{\circ}K$. In practice, the enthalpy and entropy are predicted via a thermodynamic model of duplex formation (the "nearest neighbor" model which is explained in more detail below), and used to calculate the free energy and melting temperature.

Predicted free energy of the most stable intramolecular structure of an oligonucleotide or its complement -- single-stranded DNA and RNA molecules that contain self-complementary sequences can form intramolecular secondary structures. For instance, the oligonucleotide

5' -ACTGGCAATCACAATTGCCAGTAA-3' (SEQ ID NO:1)

can base pair with itself, to form the structure

```
5' -ACTGGCAATCA
      ||||| C (SEQ ID NO:1)
3' -AATGACCGTTAA
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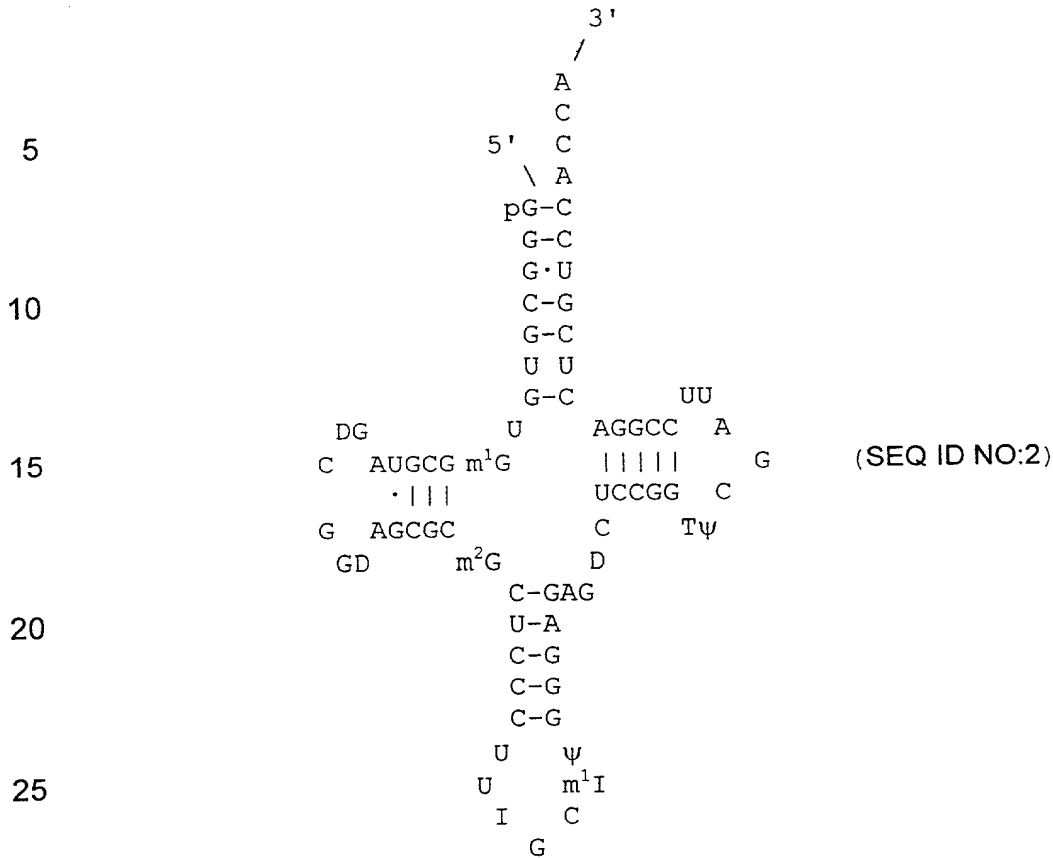
where a vertical line indicates Watson-Crick base pair formation. Many such structures are possible for a given sequence; two are of particular interest. The first is the lowest energy "hairpin" structure (formed by folding a sequence back on itself with a connecting loop at least 3 nucleotides long). The second is the lowest energy structure that can be formed by including more complex topologies, such as "bulge loops" (unpaired duplexes between two regions of base-paired duplex) and cloverleaf structures, where 3 base-paired stretches meet at a triple-junction. A good example of a complex secondary structure is the structure of a tRNA molecule, an example of which, namely, yeast tRNA^{Ala} is shown below.

For either type of structure, a value of the free energy of that structure can be calculated, relative to the unpaired strand, by means of a thermodynamic model similar to that used to calculate the free energy of a base-paired duplex structure. Again, the free energy ΔG is calculated from the enthalpy ΔH and the entropy ΔS at a given absolute temperature T via the equation

$$\Delta G = \Delta H - T \Delta S .$$

However, in this case there is the added difficulty that the lowest energy structure must be found. For a simple hairpin structure, this optimization can be performed via a relatively simple search algorithm. For more complex structures (such as a cloverleaf) a dynamic programming algorithm, such as that implemented in the program MFOLD, must be used.

Yeast tRNA^{Ala} - The RNA sequence includes many non-standard ribonucleotides, such as D (5,6 dihydrouridine), m¹G (1-methylguanosine), m²G (N²-dimethylguanosine), ψ (pseudouridine), I (inosine), m¹I (1-methylinosine) and T (ribothymidine). Dots (·) mark (non-standard) G=U base pairs. The structure is taken from A. L. Lehninger, *et al.*, Principles of Biochemistry, 2nd Ed. (Worth Publishers, New York, NY, 1993).



Coupling efficiencies -- chemosynthetic efficiencies are called coupling efficiencies when the synthetic scheme involves successive attachment of different monomers to a growing oligomer; a good example is oligonucleotide synthesis via phosphoramidite coupling chemistry.

Algorithmic Operations:

Evaluating a parameter -- determination of the numerical value of a numerical descriptor of a property of an oligonucleotide sequence by means of a formula, algorithm or look-up table.

Filter -- a mathematical rule or formula that divides a set of numbers into two subsets. Generally, one subset is retained for further analysis while the other is discarded. If the division into two subsets is achieved by testing the numbers against a simple inequality, then the filter is referred to as a "cut-off". In the context of the current invention, an example by way of illustration and not limitation is the statement "The predicted self structure free energy must be

greater than or equal to -0.4 kcal/mole," which can be used as a filter for oligonucleotide sequences; this particular filter is also an example of a cut-off.

Filter set -- A set of rules or formulae that successively winnow a set of numbers by identifying and discarding subsets that do not meet specific criteria. In the context of the current invention, an example by way of illustration and not limitation is the compound statement "the predicted self structure free energy must be greater than or equal to -0.4 kcal/mole and the predicted RNA/DNA heteroduplex melting temperature must lie between 60°C and 85°C ," which can be used as a filter set for oligonucleotide sequences.

Examining a parameter -- comparing the numerical value of a parameter to some cutoff-value or filter.

Statistical sampling of a cluster -- extraction of a subset of oligonucleotides from a cluster of oligonucleotides based upon some statistical measure, such as rank by oligonucleotide starting position in the sequence complementary to the target sequence.

First quartile, median and third quartile -- If a set of numbers is ranked by value, then the value that divides the lower $\frac{1}{4}$ from the upper $\frac{3}{4}$ of the set is the first quartile, the value that divides the set in half is the median and the value that divides the lower $\frac{3}{4}$ from the upper $\frac{1}{4}$ of the set is the third quartile.

Poorly correlated -- If it is not possible to perform a "good" prediction, as defined via statistics, of one set of numbers from another set of numbers using a simple linear model, then the two sets of numbers are said to be poorly correlated.

Computer program -- a written set of instructions that symbolically instructs an appropriately configured computer to execute an algorithm that will yield desired outputs from some set of inputs. The instructions may be written in one or several standard programming languages, such as C, C++, Visual BASIC, FORTRAN or the like. Alternatively, the instructions may be written by imposing a template onto a general-purpose numerical analysis program, such as a spreadsheet.

Experimental System Components:

Small organic molecule -- a compound of molecular weight less than 1500, preferably 100 to 1000, more preferably 300 to 600 such as biotin, fluorescein,

achieve a consensus behavior. In other words, the oligonucleotide sequences should be sufficiently numerous that several possible probes overlap or fall within a given region that is expected to yield acceptable hybridization efficiency. Since the location of these regions is not known before hand, the best strategy is to

5 equally space the probe sequences along the sequence that is hybridizable to the target sequence. Since regions of acceptable hybridization efficiency are generally on the order of 20 nucleotides in length, a practical strategy is to space the starting nucleotides of the oligonucleotide sequences no more than five basepairs apart. If computation time needed to calculate the predictive

10 parameters is not an issue, then the best strategy is to space the starting nucleotides one nucleotide apart. An important feature of the present invention is to determine oligonucleotides that are clustered along a region of the nucleotide sequence. The individual predictions made for individual oligonucleotide sequences are not very good. However, we have found that the predictions that

15 are experimentally observed tend to form contiguous clusters, while the spurious predictions tend to be solitary. Thus, the number of oligonucleotides should be sufficient to achieve the desired clustering.

Preferably, a set of overlapping sequences is chosen. To this end, the subsequences are chosen so that there is overlap of at least one nucleotide from

20 one oligonucleotide to the next. More preferably, the overlap is two or more nucleotides. Most preferably, the oligonucleotides are spaced one nucleotide apart and the predetermined number is $L-N+1$ oligonucleotides where L is the length of the nucleotide sequence and N is the length of the oligonucleotides. In the latter situation, the unique oligonucleotides are of identical length N . Thus, a

25 set of overlapping oligonucleotides is a set of oligonucleotides that are subsequences derived from some master sequence by subdividing that sequence in such a way that each subsequence contains either the start or end of at least one other subsequence in the set.

An example of the above for purposes of illustration and not limitation is presented by the sequence ATGGACTTAGCATTTCG (SEQ ID NO:3), from which the following set of overlapping oligonucleotides can be identified:

ATGGACTTAGCA (SEQ ID NO:4)
5 TGGACTTAGCAT (SEQ ID NO:5)
GGACTTAGCATT (SEQ ID NO:6)
GACTTAGCATTTC (SEQ ID NO:7)
ACTTAGCATTTCG (SEQ ID NO:8)

10 In this example the overlapping oligonucleotides are spaced one nucleotide apart. In other words, there is overlap of all but one nucleotide from one oligonucleotide to the next. In the example above, the original nucleotide sequence is 16 nucleotides long ($L=16$). The length of each of the overlapping oligonucleotides is 12 nucleotides long ($N=12$) and there are $L-N+1 = 5$ oligonucleotides.

15 The length of the oligonucleotides may be the same or different and may vary depending on the length of the nucleotide sequence. The length of the oligonucleotides is determined by a practical compromise between the limits of current chemistries for oligonucleotide synthesis and the need for longer oligonucleotides, which exhibit greater binding affinity for the target sequence and
20 are more likely to occur only once in complicated mixtures of polynucleotide targets. Usually, the length of the oligonucleotides is from about 10 to 50 nucleotides, more usually, from about 25 to 35 nucleotides.

In the next step of the method at least one parameter that is independently predictive of the ability of each of the oligonucleotides of the set to hybridize to the
25 target nucleotide sequence is determined and evaluated for each of the above oligonucleotides. Examples of such a parameter, by way of illustration and not limitation, is a parameter selected from the group consisting of composition factors, thermodynamic factors, chemosynthetic efficiencies, kinetic factors and mathematical combinations of these quantities.

30 The determination of a parameter may be carried out by known methods. For example, melting temperature of the oligonucleotide/target duplex may be determined using the nearest neighbor method and parameters appropriate for the nucleotide acids involved. For DNA/DNA parameters, see J. SantaLucia Jr., *et al.*, (1996) Biochemistry, 35:3555. For RNA/DNA parameters, see N.
35 Sugimoto, *et al.*, (1995) Biochemistry, 34:11211. Briefly, these methods are

based on the observation that the thermodynamics of a nucleic acid duplex can be modeled as the sum of a term arising from the entire duplex and a set of terms arising from overlapping pairs of nucleotides ("nearest neighbor" model). For a discussion of the nearest neighbor see J. SantaLucia Jr., *et al.*, (1996)

- 5 Biochemistry, *supra*, and N. Sugimoto, *et al.*, (1995) Biochemistry, *supra*. For example, the enthalpy ΔH of the duplex formed by the sequence

ATGGACTTAGCA (SEQ ID NO:4)

- 10 and its perfect complement can be approximated by the equation

$$\Delta H \cong H_{init} + H_{AT} + H_{TG} + H_{GG} + H_{GA} + H_{AC} \\ + H_{CT} + H_{TT} + H_{TA} + H_{AG} + H_{GC} + H_{CA} .$$

- 15 In the above equation, the term H_{init} is the initiation enthalpy for the entire duplex, while the terms H_{AT} , ..., H_{CA} are the so-called "nearest neighbor" enthalpies. Similar equations can be written for the entropy, for the corresponding quantities for RNA homoduplexes, or for DNA/RNA heteroduplexes. The free energy can then be calculated from the enthalpy, entropy and absolute temperature, as described previously.

- 20 Predicted free energy of the most stable intramolecular structure of an oligonucleotide (ΔG_{MFOLD}) may be determined using the nucleic acid folding algorithm MFOLD and parameters appropriate for the oligonucleotide, e.g., DNA or RNA. For MFOLD, see J.A. Jaeger, *et al.*, (1989), *supra*. For DNA folding parameters, see J. SantaLucia Jr., *et al.*, (1996), *supra*. Briefly, these methods
- 25 operate in two steps. First, a map of all possible compatible intramolecular base pairs is made. Second, the global minimum of the free energy of the various possible base pairing configurations is found, using the nearest neighbor model to estimate the enthalpy and entropy, the user input temperature to complete the calculation of free energy, and a dynamic programming algorithm to find the global
- 30 minimum. The algorithm is computationally intensive; calculation times scale as the third power of the sequence length.

The following Table 1 summarizes groups of parameters that are independently predictive of the ability of each of the oligonucleotides to hybridize to the target nucleotide sequence together with a reference to methods for their determination. Parameters within a given group are known or expected to be strongly correlated to one another, while parameters in different groups are known or expected to be poorly correlated with one another.

Table 1

Group	Parameter	Source or Reference
I	duplex enthalpy, ΔH	Santa Lucia <i>et al.</i> , 1996; Sugimoto <i>et al.</i> , 1995
	duplex entropy, ΔS	Santa Lucia <i>et al.</i> , 1996; Sugimoto <i>et al.</i> , 1995
	duplex free energy, ΔG	$\Delta G = \Delta H - T\Delta S$ (see text)
	melting temperature, T_m	(see text)
	mole fraction (or percent) G+C	self-explanatory
	subsequence duplex enthalpy	Santa Lucia <i>et al.</i> , 1996; Sugimoto <i>et al.</i> , 1995
	subsequence duplex entropy	Santa Lucia <i>et al.</i> , 1996; Sugimoto <i>et al.</i> , 1995
	subsequence duplex free energy	$\Delta G = \Delta H - T\Delta S$ (see text)
	subsequence duplex T_m	(see text)
	subsequence duplex mole fraction (or percent) G+C	self-explanatory
II	intramolecular enthalpy, ΔH_{MFOLD}	Jaeger <i>et al.</i> , 1989; Santa Lucia <i>et al.</i> , 1996
	intramolecular entropy, ΔS_{MFOLD}	Jaeger <i>et al.</i> , 1989; Santa Lucia <i>et al.</i> , 1996
	intramolecular free energy, ΔG_{MFOLD}	$\Delta G = \Delta H - T\Delta S$ (see text)
	hairpin enthalpy, $\Delta H_{hairpin}$	Jaeger <i>et al.</i> , 1989; Santa Lucia <i>et al.</i> , 1996
	hairpin entropy, $\Delta S_{hairpin}$	Jaeger <i>et al.</i> , 1989; Santa Lucia <i>et al.</i> , 1996
	hairpin free energy, $\Delta G_{hairpin}$	$\Delta G = \Delta H - T\Delta S$ (see text)
	intramolecular partition function, Z	$Z = \sum_{k \text{ structures}} \exp\left(-\Delta G_{\text{intramolecular}}^{(k)} / RT\right)$
III	sequence complexity	Altschul <i>et al.</i> , 1994
	sequence information content	Altschul <i>et al.</i> , 1994
IV	steric factors	molecular modeling or experiment
	molecular dynamic simulation	Weber & Hefland, 1979
	enthalpy, entropy & free energy of activation	measured experimentally
	association & dissociation rates	Patzel & Sczakiel, 1998
V	oligonucleotide chemosynthetic efficiencies	measured experimentally
VI	target synthetic efficiencies	measured experimentally

In a next step of the present method, a subset of oligonucleotides within the predetermined number of unique oligonucleotides is identified based on the above evaluation of the parameter. A number of mathematical approaches may be followed to sort the oligonucleotides based on a parameter. In one approach a cut-off value is established. The cut-off value is adjustable and can be optimized

relative to one or more training data sets. This is done by first establishing some metric for how well a cutoff value is performing; for example, one might use the normalized signal observed for each oligonucleotide in the training set. Once such a metric is established, the cutoff value can be numerically optimized to maximize the value of that metric, using optimization algorithms well known to the art. Alternatively, the cutoff value can be estimated using graphical methods, by graphing the value of the metric as a function of one or more parameters, and then establishing cutoff values that bracket the region of the graph where the chosen metric exceeds some chosen threshold value. In essence, the cut off values are chosen so that the rule set used yields training data that maximizes the inclusion of oligonucleotides that exhibit good hybridization efficiency and minimizes the inclusion of oligonucleotides that exhibit poor hybridization efficiency.

A preferred approach to performing such a graph-based optimization of filter parameters is shown in Fig. 3. In Fig. 3, hybridization data from several different genes have been used to prepare a contour plot of relative hybridization intensity as a function of DNA/RNA heteroduplex melting temperature and free energy of the most stable intramolecular structure of the probe. Contours are shown only for regions for which there are data; the white space outside of the outermost contour indicates that there are no experimental data for that region. The details of how the data were obtained can be found in Example 1 below. A summary of the sequences and number of data points employed is shown in Table 2 below. The measured hybridization intensities for each data set were normalized prior to construction of the contour plot depicted in Fig. 3 by dividing each observed intensity by the maximum intensity observed for that gene. In addition, differences in hybridization salt concentrations and hybridization temperatures were accounted for by using the salt concentration-corrected values of the melting temperatures and by subtracting the hybridization temperature from each predicted melting temperature, respectively. The filter set determined by examination of Fig. 3 is indicated by both the dotted open box in the figure and by the inequalities above the box.

One way in which such a contour plot may be prepared involves the use of an appropriate software application such as Microsoft® Excel® or the like. For

example, the cross-tabulation tool may be used in the Microsoft® Excel® program. Data is accumulated into rectangular bins that are 0.5 kcal ΔG_{MFOLD} wide and 2.5°C T_m wide. In each bin the average values of ΔG_{MFOLD} , $T_m - T_{hyb}$, and the normalized hybridization intensity are calculated. The data is output to the software application DeltaGraph® (Deltapoint, Inc., Monterey, CA) and the contour plot is prepared using the tools and instructions provided.

Table 2

Target (GenBank Accession No.)	Target Strand	No. Data Points	T_{hyb}	[Na ⁺] Correction
HIV protease-reverse transcriptase (PRT) ^a (M15654)	Sense	1,022	35°C	-1.4°C
HIV protease-reverse transcriptase (PRT) ^a (M15654)	antisense	1,041	30°C	-1.4°C
HIV protease-reverse transcriptase (PRT) ^b (M15654)	Sense	88	35°C	-1.4°C
Human G3PDH (glyceraldehyde-3-dehydrogenase) ^b (X01677)	antisense	93	35°C	-1.4°C
Human p53 ^b (X02469)	antisense	93	35°C	-1.4°C
Rabbit β -globin ^c (K03256)	antisense	106	30°C	0°C

^a Data from Affymetrix GeneChip™ Array

^b Data from biotinylated probes bound to streptavidin-coated microtiter wells

^c Literature data: see N. Milner, K. U. Mir & E. M. Southern (1997) *Nature Biotech.* **15**, 537-541.

Once the cut-off value is selected, a subset of oligonucleotides having parameter values greater than or equal to the cut-off value is identified. This refers to the inclusion of oligonucleotides in a subset based on whether the value of a predictive parameter satisfies an inequality.

Examples of identifying a subset of oligonucleotides by establishing cut-off values for predictive parameters are as follows: for melting temperature an inequality might be $60^\circ\text{C} \leq T_m$; for predicted free energy an inequality, preferably, might be

$$\Delta G_{MFOLD} \geq -0.4 \frac{\text{kcal}}{\text{mole}}.$$

In a variation of the above, both a maximum and a minimum cut-off value may be selected. A subset of oligonucleotides is identified whose values fall

within the maximum and minimum values, i.e., values greater than or equal to the minimum cut-off value and less than or equal to the maximum cut-off value. An example of this approach for melting temperature might be the inequality $60^{\circ}\text{C} \leq T_m \leq 85^{\circ}\text{C}$.

5 With regard to cut off values for T_m the lower limit is most important, and is preferably $T_m = T_{\text{hyb}}$, more preferably, $T_m = T_{\text{hyb}} + 15^{\circ}\text{C}$. The upper cutoff is important when the sequence region under consideration is unusually rich in G and C, and is preferably $T_m = T_{\text{hyb}} + 40^{\circ}\text{C}$. With regard to ΔG_{MFOLD} the cutoff value is usually greater than or equal to -1.0 kcal/mole. As mentioned above, the
10 cutoff values preferably are determined from real data through experimental observations.

 In another approach the parameter values may be converted into dimensionless numbers. The parameter value is converted into a dimensionless number by determining a dimensionless score for each parameter resulting in a
15 distribution of scores having a mean value of zero and a standard deviation of one. The dimensionless score is a number that is used to rank some object (such as an oligonucleotide) to which that score relates. A score that has no units (i.e., a pure number) is called a dimensionless score.

 In one approach the following equations are used for converting the values
20 of said parameters into dimensionless numbers:

$$s_{i,x} = \frac{x_i - \langle x \rangle}{\sigma_{\{x\}}},$$

 where $s_{i,x}$ is the dimensionless score derived from parameter x calculated for
25 oligonucleotide i , x_i is the value of parameter x calculated for oligonucleotide i , $\langle x \rangle$ is the average of parameter x calculated for all of the oligonucleotides under consideration for a given nucleotide sequence target, and $\sigma_{\{x\}}$ is the standard deviation of parameter x calculated for all of the oligonucleotides under
30 consideration for a given nucleotide sequence target, and is given by the equation

$$\sigma_{\{x\}} = \sqrt{\frac{\sum_{j=1}^M (x_j - \langle x \rangle)^2}{M-1}},$$

where M is the number of oligonucleotides. The resulting distribution of scores, {s} has a mean value of zero and a standard deviation of one. These properties can be important for a combination of the scores discussed below.

The use of a dimensionless number approach may further include calculating a combination score S_i by evaluating a weighted average of the individual values of the dimensionless scores $s_{i,x}$ by the equation:

$$S_i = \sum_{\{x\}} q_x s_{i,x},$$

where q_x is the weight assigned to the score derived from parameter x, the individual values of q_x are always greater than zero, and the sum of the weights q_x is unity.

In another variation of the above approach, the method of calculation of the composite parameter is optimized based on the correlation of the individual composite scores to real data, as explained more fully below.

In one approach the calculation of the composite score further involves determining a moving window-averaged combination score $\langle S_i \rangle$ for the i th probe by the equation:

$$\langle S_i \rangle = \frac{1}{w} \sum_{j=i-\frac{w-1}{2}}^{i+\frac{w-1}{2}} S_j, \quad w = \text{an odd integer},$$

where w is the length of the window for averaging (i.e., w nucleotides long), and then applying a cutoff filter to the value of $\langle S_i \rangle$. This procedure results in smoothing (smoothing procedure) by turning each score into a consensus metric for a set of w adjacent oligonucleotide probes. The score, referred to as the "smoothed score," is essentially continuous rather than a few discrete values. The

value of the smoothed score is strongly influenced by clustering of scores with high or low values; window averaging therefore provides a measurement of cluster size.

An advantage of the dimensionless score approach to the probe prediction algorithm is that it is easy to objectively optimize. In one approach to training the algorithm, optimization of the weights q_x above may be performed by varying the values of the weights so that the correlation coefficient $\rho_{\{<S_i>\},\{V_i\}}$ between the set of window-averaged combination scores $\{<S_i>\}$ and a set of calibration experimental measurements $\{V_i\}$ is maximized. The correlation coefficient $\rho_{\{<S_i>\},\{V_i\}}$ is calculated from the equation

$$\rho_{\{<S_i>\},\{V_i\}} = \left(\frac{1}{M} \right) \frac{\text{Covariance}(\langle S \rangle, V)}{\sigma_{\{<S_i>\}} \sigma_{\{V_i\}}},$$

where M is the number of window averaged, combination dimensionless scores and the number of corresponding measurements, the covariance is as defined earlier (see earlier equations) and $\sigma_{\{<S_i>\}}$ and $\sigma_{\{V_i\}}$ are the standard deviations of $\{<S_i>\}$ and $\{V_i\}$, as defined previously. An example of this approach is shown in Example 2, below.

In another approach the parameter is derived from one or more factors by mathematical transformation of the factors. This involves the calculation of a new predictive parameter from one or more existing predictive parameters, by means of an equation. For instance, the equilibrium constant K_{open} for formation of an oligonucleotide with no intramolecular structure from its structured form can be calculated from the intramolecular structure free energy ΔG_{MFOLD} , using the equation:

$$K_{open} = \exp\left(\frac{\Delta G_{MFOLD}}{RT}\right).$$

In a next step of the method oligonucleotides in the subset are then identified that are clustered along a region of the nucleotide sequence that is

hybridizable to the target nucleotide sequence. For example, consider a set of overlapping oligonucleotides identified by dividing a nucleotide sequence into subsequences. A subset of the oligonucleotides is obtained as described above. In general, this subset is obtained by applying a rule that rejects some members of the set. For the remaining members of the set, namely, the subset, there will be some average number of nucleotides in the nucleotide sequence between the first nucleotides of adjacent remaining subsequences. If, for some sub-region of the nucleotide sequence, the average number of nucleotides in the nucleotide sequence between the first nucleotides of adjacent remaining subsequences is less than the average for the entire nucleotide sequence, then the oligonucleotides are clustered. The smaller the average number of nucleotides between the first nucleotides of adjacent oligonucleotides, the stronger the clustering. The strongest clustering occurs when there are no intervening nucleotides between adjacent starting nucleotides. In this case, the oligonucleotides are said to be contiguous and may be referred to as contiguous sequence elements or "contigs."

Accordingly, in this step oligonucleotides are sorted based on length of contiguous sequence elements. Oligonucleotides in the subset determined above are identified that are contiguous along a region of the input nucleic acid sequence. The length of each contig that is equal to the number of oligonucleotides in each contig, namely, oligonucleotides from the above step whose complement begin at positions $m+1$, $m+2$, ..., $m+k$ in the target sequence, form a contig of length k . Contigs can be identified and contig length can be calculated using, for example, a Visual Basic® module that can be incorporated into a Microsoft® Excel workbook.

Cluster size can be defined in several ways:

For contiguous clusters, the size is simply the number of adjacent oligonucleotides in the cluster. Again, this may also be referred to as contiguous sequence elements. The number may also be referred to as "contig length". For example, consider the nucleotide sequence discussed above, namely, ATGGACTTAGCATTCG (SEQ ID NO:3) and the identified set of overlapping oligonucleotides

rhodamine and other dyes, tetracycline and other protein binding molecules, and haptens, *etc.* The small organic molecule can provide a means for attachment of a nucleotide sequence to a label or to a support.

Support or surface -- a porous or non-porous water insoluble material. The surface can have any one of a number of shapes, such as strip, plate, disk, rod, particle, including bead, and the like. The support can be hydrophilic or capable of being rendered hydrophilic and includes inorganic powders such as glass, silica, magnesium sulfate, and alumina; natural polymeric materials, particularly cellulosic materials and materials derived from cellulose, such as fiber containing papers, e.g., filter paper, chromatographic paper, etc.; synthetic or modified naturally occurring polymers, such as nitrocellulose, cellulose acetate, poly (vinyl chloride), polyacrylamide, cross linked dextran, agarose, polyacrylate, polyethylene, polypropylene, poly(4-methylbutene), polystyrene, polymethacrylate, poly(ethylene terephthalate), nylon, poly(vinyl butyrate), etc.; either used by themselves or in conjunction with other materials; glass available as Bioglass, ceramics, metals, and the like. Natural or synthetic assemblies such as liposomes, phospholipid vesicles, and cells can also be employed.

Binding of oligonucleotides to a support or surface may be accomplished by well-known techniques, commonly available in the literature. See, for example, A. C. Pease, *et al.*, Proc. Nat. Acad. Sci. USA, 91:5022-5026 (1994).

Label -- a member of a signal producing system. Usually the label is part of a target nucleotide sequence or an oligonucleotide probe, either being conjugated thereto or otherwise bound thereto or associated therewith. The label is capable of being detected directly or indirectly. Labels include (i) reporter molecules that can be detected directly by virtue of generating a signal, (ii) specific binding pair members that may be detected indirectly by subsequent binding to a cognate that contains a reporter molecule, (iii) oligonucleotide primers that can provide a template for amplification or ligation or (iv) a specific polynucleotide sequence or recognition sequence that can act as a ligand such as for a repressor protein, wherein in the latter two instances the oligonucleotide primer or repressor protein will have, or be capable of having, a reporter molecule. In general, any reporter molecule that is detectable can be used.

The reporter molecule can be isotopic or nonisotopic, usually non-isotopic, and can be a catalyst, such as an enzyme, a polynucleotide coding for a catalyst, promoter, dye, fluorescent molecule, chemiluminescent molecule, coenzyme, enzyme substrate, radioactive group, a small organic molecule, amplifiable
5 polynucleotide sequence, a particle such as latex or carbon particle, metal sol, crystallite, liposome, cell, etc., which may or may not be further labeled with a dye, catalyst or other detectable group, and the like. The reporter molecule can be a fluorescent group such as fluorescein, a chemiluminescent group such as luminol, a terbium chelator such as N-(hydroxyethyl) ethylenediaminetriacetic acid
10 that is capable of detection by delayed fluorescence, and the like.

The label is a member of a signal producing system and can generate a detectable signal either alone or together with other members of the signal producing system. As mentioned above, a reporter molecule can be bound directly to a nucleotide sequence or can become bound thereto by being bound to
15 an sbp member complementary to an sbp member that is bound to a nucleotide sequence. Examples of particular labels or reporter molecules and their detection can be found in U.S. Patent No. 5,508,178 issued April 16, 1996, at column 11, line 66, to column 14, line 33, the relevant disclosure of which is incorporated herein by reference. When a reporter molecule is not conjugated to a nucleotide
20 sequence, the reporter molecule may be bound to an sbp member complementary to an sbp member that is bound to or part of a nucleotide sequence.

Signal Producing System -- the signal producing system may have one or more components, at least one component being the label. The signal producing
25 system generates a signal that relates to the presence or amount of a target polynucleotide in a medium. The signal producing system includes all of the reagents required to produce a measurable signal. Other components of the signal producing system may be included in a developer solution and can include substrates, enhancers, activators, chemiluminescent compounds, cofactors,
30 inhibitors, scavengers, metal ions, specific binding substances required for binding of signal generating substances, and the like. Other components of the signal producing system may be coenzymes, substances that react with enzymic products, other enzymes and catalysts, and the like. The signal producing system

provides a signal detectable by external means, by use of electromagnetic radiation, desirably by visual examination. Signal-producing systems that may be employed in the present invention are those described more fully in U.S. Patent No. 5,508,178, the relevant disclosure of which is incorporated herein by
5 reference.

Ancillary Materials -- Various ancillary materials will frequently be employed in the methods and assays utilizing oligonucleotide probes designed in accordance with the present invention. For example, buffers and salts will normally be present in an assay medium, as well as stabilizers for the assay
10 medium and the assay components. Frequently, in addition to these additives, proteins may be included, such as albumins, organic solvents such as formamide, quaternary ammonium salts, polycations such as spermine, surfactants, particularly non-ionic surfactants, binding enhancers, e.g., polyalkylene glycols, or the like.

15 DETAILED DESCRIPTION OF THE INVENTION

The invention is directed to methods or algorithms for predicting oligonucleotides specific for a nucleic acid target where the oligonucleotides exhibit a high potential for hybridization. The algorithm uses parameters of the oligonucleotide and the oligonucleotide/target nucleotide sequence duplex, which
20 can be readily predicted from the primary sequences of the target polynucleotide and candidate oligonucleotides. In the methods of the present invention, oligonucleotides are filtered based on one or more of these parameters, then further filtered based on the sizes of clusters of oligonucleotides along the input polynucleotide sequence. The methods or algorithms of the present invention
25 may be carried out using either relatively simple user-written subroutines or publicly available stand-alone software applications (e.g., dynamic programming algorithm for calculating self-structure free energies of oligonucleotides). The parameter calculations may be orchestrated and the filtering algorithms may be implemented using any of a number of commercially available computer programs
30 as a framework such as, e.g., Microsoft® Excel spreadsheet, Microsoft® Access relational database and the like. The basic steps involved in the present methods involve parsing a sequence that is complementary to a target nucleotide sequence into a set of overlapping oligonucleotide sequences, evaluating one or more

parameters for each of the oligonucleotide sequences, said parameter or parameters being predictive of probe hybridization to the target nucleotide sequence, filtering the oligonucleotide sequences based on the values for each parameter, filtering the oligonucleotide sequences based on the length of contiguous sequence elements and ranking the contiguous sequence elements based on their length. We have found that oligonucleotides in the longest contiguous sequence elements generally show the highest hybridization efficiencies.

The present methods are based on our recognition that oligonucleotides showing high hybridization efficiencies tend to form clusters. It is believed that this clustering reflects local regions of the target nucleotide sequence that are unstructured and accessible for oligonucleotide binding. Oligonucleotides that are contiguous along a region of the input nucleic acid sequence are identified. These oligonucleotides are sorted based on the length of the contiguous sequence elements. The sorting approach used in the present invention apparently serves as a surrogate for the calculation of local secondary structure of the target nucleotide sequence. This is supported by our observation that treatments intended to eliminate long-range nucleic acid structure (e.g., random fragmentation) do not eliminate the differences in hybridization yields across oligonucleotide probe arrays. This implies that major determinants of efficient hybridization are local regions of the target sequence. The identification of contiguous sequence elements is a simple and efficient method for recognizing clusters of such determinants and, thus, for identifying oligonucleotide probes that exhibit high hybridization efficiency for a target nucleotide sequence.

As mentioned above one embodiment of the present invention is a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides is identified. The length of the oligonucleotides may be the same or different. The oligonucleotides are unique in that no two of the oligonucleotides are identical. The unique oligonucleotides are chosen to sample the entire length of a nucleotide sequence that is hybridizable with the target nucleotide sequence. The actual number of oligonucleotides is generally determined by the length of the nucleotide sequence and the desired result. The number of oligonucleotides should be sufficient to

ATGGACTTAGCA (SEQ ID NO:4)
TGGACTTAGCAT (SEQ ID NO:5)
GGACTTAGCATT (SEQ ID NO:6)
GACTTAGCATTC (SEQ ID NO:7)
5 ACTTAGCATTCG (SEQ ID NO:8)

Suppose that, after calculation and evaluation of the predictive parameters, four nucleotides remain:

10	ATGGACTTAGCA	(SEQ ID NO:4)		contig
	TGGACTTAGCAT	(SEQ ID NO:5)		
	GGACTTAGCATT	(SEQ ID NO:6)		
	ACTTAGCATTCG	(SEQ ID NO:8)		single oligonucleotide

15 A "contig" encompassing three of the oligonucleotides of the subset is present together with a single oligonucleotide. The contig length is 3 oligonucleotides.

Alternatively, cluster size at some position in the sequence hybridizable or complementary to the target sequence may be defined as the number of oligonucleotides whose center nucleotides fall inside a region of length M

20 centered about the position in question, divided by M. This definition of clustering allows small gaps in clusters. In the example used above for contiguous clusters, if M was 10, then the cluster size would step through the values 0/10,..., 0/10, 1/10, 2/10, 3/10, 3/10, 4/10, 4/10, 4/10, 4/10, 4/10, 3/10, 2/10, 1/10, 1/10, 0/10 as the center of the window of length 10 passed through the cluster. In each fraction,

25 the numerator is the number of oligonucleotide sequences that have satisfied the filter set and whose central nucleotides are within a window 10 nucleotides long, centered about the nucleotide under consideration. The denominator (10) is simply the window length.

Another alternative is to define the size of a cluster at some position in the

30 sequence hybridizable or complementary to the target sequence as the number of oligonucleotide sequences overlapping that position. This definition is equivalent to the last definition with M set equal to the oligonucleotide probe length and omission of the division by M.

Finally, cluster size can be approximated at each position in a nucleotide

35 sequence by dividing the sequence into oligonucleotides, evaluating a numerical score for each oligonucleotide, and then averaging the scores in the neighborhood

of each position by means of a moving window average as described above. Window averaging has the effect of reinforcing clusters of high or low values around a particular position, while canceling varying values about that position. The window average, therefore, provides a score that is sensitive to both the
5 hybridization potential of a given oligonucleotide and the hybridization potentials of its neighbors.

In a next step of the present method, the oligonucleotides in the subset are ranked. Generally, this ranking is based on the lengths of the clusters or contigs, sizes of the clusters or values of a window averaged score. Oligonucleotides
10 found in the longest contigs or largest clusters, or possessing the highest window averaged scores usually show the highest hybridization efficiencies. Often, the highest signal intensity within the cluster corresponds to the median oligonucleotide of the cluster. However, the peak signal intensity within the contig can be determined experimentally, by sampling the cluster at its first quartile,
15 midpoint and third quartile, measuring the hybridization efficiencies of the sampled oligonucleotides, interpolating or extrapolating the results, predicting the position of the optimal probe, and then iterating the probe design process.

Fig. 1 shows a diagram of an example of the above-described method by way of illustration and not limitation. Referring to Fig. 1 a target sequence of
20 length L from, e.g., a database, is used to generate a sequence that is hybridizable to the target sequence from which candidate oligonucleotide probe sequences are generated. One or more parameters are calculated for each of the oligonucleotide probe sequences. The candidate oligonucleotide probe sequences are filtered based on the values of the parameters. Clustering of the
25 filtered candidate probe sequences is evaluated and the clusters are ranked by size. Then, the oligonucleotide probes are statistically sampled and synthesized. Further evaluation may be made by evaluating the hybridization of the selected oligonucleotide probes in real hybridization experiments. The above process may be reiterated to further define the selection. In this way only a small fraction of the
30 potential oligonucleotide probe candidates are synthesized and tested. This is in sharp contrast to the known method of synthesizing and testing all or a major portion of potential oligonucleotide probes for a given target sequence.

The methods of the present invention are preferably carried out at least in part with the aid of a computer. For example, an IBM® compatible personal computer (PC) may be utilized. The computer is driven by software specific to the methods described herein.

5 The preferred computer hardware capable of assisting in the operation of the methods in accordance with the present invention involves a system with at least the following specifications: Pentium® processor or better with a clock speed of at least 100 MHz, at least 32 megabytes of random access memory (RAM) and at least 80 megabytes of virtual memory, running under either the Windows 95 or
10 Windows NT 4.0 operating system (or successor thereof).

As mentioned above, software that may be used to carry out the methods may be either Microsoft Excel or Microsoft Access, suitably extended via user-written functions and templates, and linked when necessary to stand-alone programs that calculate specific parameters (e.g., MFOLD for intramolecular
15 thermodynamic parameters). Examples of software programs used in assisting in conducting the present methods may be written, preferably, in Visual BASIC, FORTRAN and C++, as exemplified below in the Examples. It should be understood that the above computer information and the software used herein are by way of example and not limitation. The present methods may be adapted to
20 other computers and software. Other languages that may be used include, for example, PASCAL, PERL or assembly language.

Fig. 2 depicts a more specific approach to a method in accordance with the present invention. Referring to Fig. 2, a sequence of length L is obtained from a database such as GenBank, UniGene or a proprietary sequence database. Probe
25 length N is determined by the user based on the requirements for sensitivity and specificity and the limitations of the oligonucleotide synthetic scheme employed. The probe length and sequence length are used to generate L-N+1 candidate oligonucleotide probes, i.e., from every possible starting position. An initial selection is made based on local sequence predicted thermodynamic properties.
30 To this end, melting temperature T_m and the self-structure free energy ΔG_{MFOLD} , are calculated for each of the potential oligonucleotide probe: target nucleotide sequence complexes. Next, M probes that satisfy T_m and ΔG_{MFOLD} filters are selected. A further selection can be made based on clustering of "good"

parameters. Good parameters are parameters that satisfy all of the filters in the filter set. Clustering is defined by any of the methods described previously; in Fig. 2, the "contig length" definition of clustering is used.

For each of the M oligonucleotide sequences that satisfied all filters the question is asked whether the oligonucleotide sequence immediately following the sequence under consideration is also one of the sequences that satisfied all of the filters. If the answer to this question is NO, then one stores the current value of the contig length counter, resets the counter to zero and proceeds to the next oligonucleotide sequence that satisfied all filters. If the answer to the question is YES, then 1 is added to the contig length counter and, if the counter now equals 1 (i.e., this is the first oligonucleotide probe sequence in the contig), the starting position of the oligonucleotide is stored. One then moves to the next oligonucleotide that satisfied all filters, which, in this case, is the same as the next oligonucleotide before the application of the filter set. The process is repeated until all M filtered oligonucleotide sequences have been examined. In this way, a single pass through the set of M filtered oligonucleotide sequences generates the lengths and starting positions of all contigs.

Next, contigs are ranked based on the lengths of their contiguous sequence elements. Longer contig lengths generally correlate with higher hybridization efficiencies. All oligonucleotides of the higher-ranking contigs may be considered, or candidate oligonucleotide probes may be picked. For example, candidate oligonucleotide probes can be picked one quarter, one half and three quarters of the way through each contig. The latter approach provides local curvature determination after experimental determination of hybridization efficiencies, which allows either interpolation or extrapolation of the positions of the next probes to be synthesized in order to close in on the optimal probe in the region. If the contig brackets the actual peak of hybridization efficiency, the process will converge in 2-3 iterations. If the contig lies to one side of the actual peak, the process will converge in 3-4 iterations.

The above illustrative approach is further described with reference to the following DNA nucleotide sequence, which is the complement of the target RNA nucleotide sequence:

GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA
(SEQ ID NO:9).

5 In the first step of the method, the nucleotide sequence is divided into overlapping oligonucleotides that are 25 nucleotides in length. This length is chosen because it is an effective compromise between the need for sensitivity (enhanced by longer oligonucleotides) and the chemosynthetic efficiency of schemes for synthesis of surface-bound arrays of oligonucleotide probes.

10 Next, the estimated duplex melting temperatures (T_m) and self-structure free energies (ΔG_{MFOLD}) are calculated for each oligonucleotide in the set of overlapping oligonucleotides. The values are obtained from a user-written function that calculates DNA/RNA heteroduplex thermodynamic parameters (see N. Sugimoto, *et al.*, Biochemistry, 34:11211 (1995)) and a modified version of the program MFOLD that estimates the free energy of the most stable intramolecular

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structure of a single stranded DNA molecule (see J.A. Jaeger, *et al.*, (1989), *supra*, respectively. The steps are illustrated below.

5 GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA (target complement sequence)

		T_m (°C)	ΔG_{MFOLD}	
	GTCCAAAAGGGTCAGTCTACCTCC	71.77	-1.20	SEQ ID NO:10
10	TCCAAAAGGGTCAGTCTACCTCCC	71.99	-1.20	SEQ ID NO:11
	CCAAAAGGGTCAGTCTACCTCCCG	70.78	-1.20	SEQ ID NO:12
	CAAAAGGGTCAGTCTACCTCCCGC	71.23	-1.20	SEQ ID NO:13
	AAAAAGGGTCAGTCTACCTCCCGCC	73.07	-1.20	SEQ ID NO:14
	AAAAGGGTCAGTCTACCTCCCGCCA	75.68	-1.20	SEQ ID NO:15
15	AAAGGGTCAGTCTACCTCCCGCCAT	77.53	-1.20	SEQ ID NO:16
	AAGGGTCAGTCTACCTCCCGCCATA	79.03	-1.20	SEQ ID NO:17
	AGGGTCAGTCTACCTCCCGCCATAA	79.03	-1.20	SEQ ID NO:18
	GGGTCAGTCTACCTCCCGCCATAAA	76.85	-1.20	SEQ ID NO:19
	GGTCAGTCTACCTCCCGCCATAAAA	73.10	-0.80	SEQ ID NO:20
20	GTCAGTCTACCTCCCGCCATAAAAA	69.50	0.90	SEQ ID NO:21
	TCAGTCTACCTCCCGCCATAAAAAA	65.60	0.90	SEQ ID NO:22
	CAGTCTACCTCCCGCCATAAAAAAC	64.96	0.90	SEQ ID NO:23
	AGTCTACCTCCCGCCATAAAAAACT	65.	1.10	SEQ ID NO:24
	GTCTACCTCCCGCCATAAAAAACTC	66.36	2.40	SEQ ID NO:25
25	TCTACCTCCCGCCATAAAAAACTCA	64.97	2.90	SEQ ID NO:26
	CTACCTCCCGCCATAAAAAACTCAT	63.96	2.70	SEQ ID NO:27
	TACCTCCCGCCATAAAAAACTCATG	62.58	1.10	SEQ ID NO:28
	ACCTCCCGCCATAAAAAACTCATGT	65.10	0.40	SEQ ID NO:29
	CCTCCCGCCATAAAAAACTCATGTT	64.96	0.10	SEQ ID NO:30
30	CTCCCGCCATAAAAAACTCATGTTT	63.37	-0.10	SEQ ID NO:31
	TCCCGCCATAAAAAACTCATGTTCA	62.86	-0.10	SEQ ID NO:32
	CCCGCCATAAAAAACTCATGTTCAA	60.47	-0.10	SEQ ID NO:33
	CCGCCATAAAAAACTCATGTTCAAG	57.98	-0.10	SEQ ID NO:34
35	CGCCATAAAAAACTCATGTTCAAGA	56.20	-0.10	SEQ ID NO:35

Next, the oligonucleotide sequences are filtered on the basis of T_m . A high and low cut-off value may be selected, for example, $60^\circ\text{C} \leq T_m \leq 85^\circ\text{C}$. Thus, oligonucleotides having T_m values falling within the above range are retained. Those outside the range are discarded, which is indicated below by lining out of

5 those oligonucleotides and parameter values.

GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA (target complement sequence)

		T_m ($^\circ\text{C}$)	ΔG_{MFOLD}
10	GTCCAAAAGGGTCAGTCTACCTCC	71.77	-1.20
	TCCAAAAGGGTCAGTCTACCTCCC	71.99	-1.20
	CCAAAAGGGTCAGTCTACCTCCC	70.78	-1.20
	CAAAAAGGGTCAGTCTACCTCCCGC	71.23	-1.20
15	AAAAAGGGTCAGTCTACCTCCCGCC	73.07	-1.20
	AAAAGGGTCAGTCTACCTCCCGCCA	75.68	-1.20
	AAAGGGTCAGTCTACCTCCCGCCAT	77.53	-1.20
	AAGGGTCAGTCTACCTCCCGCCATA	79.03	-1.20
	AGGGTCAGTCTACCTCCCGCCATAA	79.03	-1.20
20	GGGTCAGTCTACCTCCCGCCATAAA	76.85	-1.20
	GGTCAGTCTACCTCCCGCCATAAAA	73.10	-0.80
	GTCAGTCTACCTCCCGCCATAAAAA	69.50	0.90
	TCAGTCTACCTCCCGCCATAAAAAA	65.60	0.90
	CAGTCTACCTCCCGCCATAAAAAAC	64.96	0.90
25	AGTCTACCTCCCGCCATAAAAAACT	65.48	1.10
	GTCTACCTCCCGCCATAAAAAACTC	66.36	2.40
	TCTACCTCCCGCCATAAAAAACTCA	64.97	2.90
	CTACCTCCCGCCATAAAAAACTCAT	63.96	2.70
	TACCTCCCGCCATAAAAAACTCATG	62.58	1.10
30	ACCTCCCGCCATAAAAAACTCATGT	65.10	0.40
	CCTCCCGCCATAAAAAACTCATGTT	64.96	0.10
	CTCCCGCCATAAAAAACTCATGTTC	63.37	-0.10
	TCCCGCCATAAAAAACTCATGTTCA	62.86	-0.10
	CCCGCCATAAAAAACTCATGTTCAA	60.47	-0.10
35	CGGGCATAAAAAACTCATGTTCAAG	57.98	-0.10
	CGGCATAAAAAACTCATGTTCAAGA	56.20	-0.10

Next, the oligonucleotide sequences remaining after the above exercise are filtered on the basis of ΔG_{MFOLD} and are retained if the value is greater than - 0.4. Those oligonucleotides with a ΔG_{MFOLD} less than - 0.4 are discarded, which is indicated below by double lining out of those oligonucleotides and parameter values.

GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA (target complement sequence)

10

	T_m (°C)	ΔG_{MFOLD}
GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	71.77	-1.20
TCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	71.99	-1.20
GCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	70.78	-1.20
CAAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	71.23	-1.20
AAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	73.07	-1.20
AAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	75.68	-1.20
AAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	77.53	-1.20
AAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	79.03	-1.20
AGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	79.03	-1.20
GCGTCACTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	76.85	-1.20
GCTCACTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	73.10	-0.80
GTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	69.50	0.90
TCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	65.60	0.90
CAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	64.96	0.90
AGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	65.48	1.10
GTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	66.36	2.40
TCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	64.97	2.90
CTACCTCCCGCCATAAAAAACTCATGTTCAAGA	63.96	2.70
TACCTCCCGCCATAAAAAACTCATGTTCAAGA	62.58	1.10
ACCTCCCGCCATAAAAAACTCATGTTCAAGA	65.10	0.40
CCTCCCGCCATAAAAAACTCATGTTCAAGA	64.96	0.10
CTCCCGCCATAAAAAACTCATGTTCAAGA	63.37	-0.10
TCCCGCCATAAAAAACTCATGTTCAAGA	62.86	-0.10
CCCGCCATAAAAAACTCATGTTCAAGA	60.47	-0.10
CGCCATAAAAAACTCATGTTCAAGA	57.98	-0.10
CGCCATAAAAAACTCATGTTCAAGA	56.20	-0.10

35

Clusters of retained oligonucleotides are identified and ranked based on cluster size. In this example, a contiguous cluster of 13 retained oligonucleotides is identified by the vertical black bar on the left. Any or all of the oligonucleotides in this cluster may be evaluated experimentally.

GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA

(target complement sequence)

		T_m (°C)	ΔG_{MFOLD}
10	GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	71.77	-1.20
	TGGAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	71.99	-1.20
	CGAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	70.78	-1.20
	CAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	71.23	-1.20
15	AAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	73.07	-1.20
	AAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	75.68	-1.20
	AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	77.53	-1.20
	AAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	79.03	-1.20
	AGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	79.03	-1.20
20	GGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	76.85	-1.20
	GCTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	73.10	-0.80
	GTCAAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	69.50	0.90
	TCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	65.60	0.90
25	CAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	64.96	0.90
	AGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	65.48	1.10
	GTCTACCTCCCGCCATAAAAACTCATGTTCAAGA	66.36	2.40
	TCTACCTCCCGCCATAAAAACTCATGTTCAAGA	64.97	2.90
	CTACCTCCCGCCATAAAAACTCATGTTCAAGA	63.96	2.70
30	TACCTCCCGCCATAAAAACTCATGTTCAAGA	62.58	1.10
	ACCTCCCGCCATAAAAACTCATGTTCAAGA	65.10	0.40
	CCTCCCGCCATAAAAACTCATGTTCAAGA	64.96	0.10
	CTCCCGCCATAAAAACTCATGTTCAAGA	63.37	-0.10
	TCCCGCCATAAAAACTCATGTTCAAGA	62.86	-0.10
35	CCCGCCATAAAAACTCATGTTCAAGA	60.47	-0.10
	CCCCATAAAAACTCATGTTCAAGA	57.98	-0.10
	GGCCATAAAAACTCATGTTCAAGA	56.20	-0.10

Alternatively, in one approach the oligonucleotides at the first quartile, the median and the third quartile of the cluster may be selected for experimental evaluation, indicated below by bold print.

5

GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA (target complement sequence)

		T_m (°C)	ΔG_{MFOLD}
10	GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	71.77	-1.20
	TCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	71.99	-1.20
	GCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	70.78	-1.20
	CAAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	71.23	-1.20
	AAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	73.07	-1.20
15	AAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	75.68	-1.20
	AAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	77.53	-1.20
	AGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	79.03	-1.20
	AGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	79.03	-1.20
	GGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	76.85	-1.20
20	GTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	73.10	-0.90
	GTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	69.50	0.90
	TACCTCCCGCCATAAAAAACTCATGTTCAAGA	65.60	0.90
	CAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	64.96	0.90
25	AGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	65.48	1.10
	GTCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	66.36	2.40
	TCTACCTCCCGCCATAAAAAACTCATGTTCAAGA	64.97	2.90
	CTACCTCCCGCCATAAAAAACTCATGTTCAAGA	63.96	2.70
	TACCTCCCGCCATAAAAAACTCATGTTCAAGA	62.58	1.10
	ACCTCCCGCCATAAAAAACTCATGTTCAAGA	65.10	0.40
30	CCTCCCGCCATAAAAAACTCATGTTCAAGA	64.96	0.10
	CTCCCGCCATAAAAAACTCATGTTCAAGA	63.37	-0.10
	TCCCGCCATAAAAAACTCATGTTCAAGA	62.86	-0.10
	CCCGCCATAAAAAACTCATGTTCAAGA	60.47	-0.10
	CCCGCCATAAAAAACTCATGTTCAAGA	57.98	-0.10
35	CGCCATAAAAAACTCATGTTCAAGA	56.20	-0.10

In one aspect of the present method, at least two parameters are determined wherein the parameters are poorly correlated with respect to one another. The reason for requiring that the different parameters chosen are poorly correlated with one another is that an additional parameter that is strongly correlated to the original parameter brings no additional information to the prediction process. The correlation to the original parameter is a strong indication that both parameters represent the same physical property of the system. Another way of stating this is that correlated parameters are linearly dependent on one another, while poorly correlated parameters are linearly independent of one another. In practice, the absolute value of the correlation coefficient between any two parameters should be less than 0.5, more preferably, less than 0.25, and, most preferably, as close to zero as possible.

In one preferred approach instead of T_m , for each oligonucleotide/target nucleotide sequence duplex, the difference between the predicted duplex melting temperature corrected for salt concentration and the temperature of hybridization of each of the oligonucleotides with the target nucleotide sequence is determined.

5 In one aspect the present method comprises determining two parameters at least one of the parameters being the association free energy between a subsequence within each of the oligonucleotides and its complementary sequence on the target nucleotide sequence, or some similar, strongly correlated parameter. The object of this approach is to identify a particularly stable subsequence of the
10 oligonucleotide that might be capable of acting as a nucleation site for the beginning of the heteroduplex formation between the oligonucleotide and the target nucleotide sequence. Such nucleation is believed to be the rate-limiting step for process of heteroduplex formation.

The subsequence within the oligonucleotide is from about 3 to 9
15 nucleotides in length, usually, 5 to 7 nucleotides in length. The subsequence is at least three nucleotides from the terminus of the oligonucleotide. For support-bound oligonucleotides the subsequence is at least three nucleotides from the free end of the oligonucleotide, i.e., the end that is not attached to the support. Generally, this free end is the 5' end of the oligonucleotide. When the
20 oligonucleotide is attached to a support, the subsequence is at least three nucleotides from the end of the oligonucleotide that is bound to the surface of the support to which the oligonucleotide is attached. Generally, the 3' end of the oligonucleotide is bound to the support.

The predictive parameter can be, for example, either melting temperature
25 or duplex free energy of the subsequence with the target nucleotide sequence. The subsequence with the maximum (melting temperature) or minimum (free energy) value of one of the above parameters is chosen as the representative subsequence for that oligonucleotide probe. For example, if the oligonucleotide is 20 nucleotides in length and a subsequence of 5 nucleotides is chosen, i.e., a 5-
30 mer, then parameter values are calculated for all 5-mer subsequences of the oligonucleotide that do not include the 2 nucleotides at the free end of the oligonucleotide. Where 5' is the free end of the oligonucleotide with designated nucleotide number 1, the values are calculated for all 5-mer subsequences with

starting nucleotides from position number 3 to position number 16. Thus, in this example, parameter values for 14 different subsequences are calculated. The subsequence with the maximum value for the parameter is then assigned as the stability subsequence for the oligonucleotide.

5 The inclusion of the above determination of a stability subsequence results in the following algorithm for determining the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides are identified within a nucleotide sequence that is hybridizable with said target nucleotide sequence. The oligonucleotides are chosen to sample
10 the entire length of the nucleotide sequence. For each of the oligonucleotides, parameters that are independently predictive of the ability of each of said oligonucleotides to hybridize to said target nucleotide sequence are determined and evaluated. Two parameters that may be used are the thermodynamic parameters of T_m and ΔG_{MFOLD} . These parameters give rise to associated
15 parameter filters. In one approach evaluation of the parameters involves establishing cut-off values as described above. Application of these cut-off values results in the identification of a subset of oligonucleotides for further scrutiny under the algorithm. In accordance with this embodiment of the present invention, there is included a stability subsequence limit in addition to the above. Cutoff values
20 are determined either by means of objective optimization algorithms well known to the art or via graphical estimation methods; both approaches have been described previously in this document. In either case, the optimization of cutoff values involves comparison of predictions to known hybridization efficiency data sets. This process results in objective optimization as it looks at prediction versus
25 experimental results and is otherwise referred to herein as "training the algorithm." The experimental data used to train the algorithm is referred to herein as "training data."

 In the present approach filters are assigned to the T_m oligonucleotide probe data. The T_m of each oligonucleotide probe needs to be greater than or equal to
30 the assigned filter (T_m probe limit) to be given a filter score of "1"; otherwise, the filter score is "0". In addition, one can also impose a second filter for this parameter; that is, that the T_m of the oligonucleotide probe also has to be less than a defined upper limit. Filters are also assigned to the ΔG_{MFOLD} data. The

ΔG_{MFOLD} of each oligonucleotide probe should be greater than or equal to the assigned filter (ΔG_{MFOLD} limit) to be given a filter score of "1"; otherwise, the filter score is "0". The filter scores are added. Furthermore, one can also impose a second filter for this parameter; that is, that the ΔG_{MFOLD} also has to be less than a defined upper limit. In accordance with the above discussion stability subsequences are identified. This leads to another filter. Accordingly, filters are assigned to the stability sequence data. The stability subsequence of each oligonucleotide probe needs to be greater than or equal to the assigned filter limit to be given a filter score of "1"; otherwise, the filter score is "0". In addition, one can also impose a second filter for this parameter; that is, that the stability subsequence also has to be less than a defined upper limit. In all cases, the filter values are determined by objective optimization (algorithmic or graphical) of the predictions of the present method versus training data, as described previously.

On the basis of the above filter sets a subset of oligonucleotides within said predetermined number of unique oligonucleotides is identified. Oligonucleotides in the subset are identified that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence. The resulting number of oligonucleotide probe regions is examined. The above filters may then be loosened or tightened by changing the filter limits to obtain more or fewer clusters of oligonucleotides to match the goal, which is set by the needs of the investigator. For instance, a particular application might require that the investigator design 5 non-overlapping probes that efficiently hybridize to a given target sequence.

As mentioned above, the contigs may be selected on the basis of contig length. In another approach, the scores defined above may be summed for cluster size determination. To this end the probe score of the particular filter set (e.g., T_m probe limit, ΔG_{MFOLD} limit and stability sequence limit) is calculated for each oligonucleotide probe. The probe score is the sum of the filter scores. Thus, the probe score is 0 if no parameters pass their respective filters. The probe score is 1, 2 or 3 if one, two or three parameters, respectively, pass their filters for that oligonucleotide probe. This summing is continued for each parameter that is in the current filter set of the algorithm used. For a given algorithm a minimum probe score limit is set. In the current example this limit will be at least 1 and could be 2

or 3 depending on the needs of the investigator, the number of probe clusters required and the results of objective optimizations of algorithm performance against training data. The probe score is compared to this probe score limit. If the probe score of oligonucleotide probe i is greater than or equal to the probe score limit, then oligonucleotide probe i is assigned a score passed value of 1. Next, a window is chosen for the evaluation of clustering (the "cluster window"). This will be the next filter applied. The cluster window (" w ") smooths the score passed values by summing the values in a window w nucleotides long, centered about position i . The resulting sum is called the cluster sum. Usually, the cluster window is an odd integer, usually 7 or 9 nucleotides. The cluster sum values are then filtered, by comparing to a user-set threshold, cluster filter. If cluster sum is greater than or equal to cluster filter, this filter is passed, and the probe is predicted to hybridize efficiently to its target.

This window summing procedure converts the score for the passed value for each oligonucleotide into a consensus metric for a set of w adjacent probes. A "consensus metric" is a measurement that distills a number of values into one consensus value. In this case, the consensus value is calculated by simply summing the individual values. The window summing procedure therefore evaluates a property similar to the contig length metric discussed above. However, the summed score has the advantage of allowing for a few probes within a cluster to have not passed their individual probe score limits. We have found that this allows more observed hybridization peaks to be predicted.

It may be desired in some circumstances to combine the results of multiple algorithm versions. We refer to this operation as "tiling". This may be explained more fully as follows. Tiling generally involves joining together the predicted oligonucleotide probe sets identified by multiple algorithm versions. In the context of the present invention, tiling multiple algorithm versions involves forming the union of multiple sets of predictions. These predictions may arise from different embodiments of the present invention. Alternatively, the different sets of predictions may arise from the same embodiment, but different filter sets. The different filter sets may additionally be restricted to different combinations of parameter values. For instance, one filter set might be used when the predicted

duplex melting temperature T_m is greater than or equal to some value, while another might be used when T_m is below that value.

An example of the logical endpoint of tiling multiple filter sets across different regions of the possible combinations of predictive parameters and then
5 forming the union of the resulting predictions is the contour plot shown in Fig. 3, with the associated rule that "the value of the normalized hybridization intensity associated with a particular combination of $(T_m - T_{hyb})$ and ΔG_{MFOLD} must be greater than or equal to some threshold value." In this case, the contour at the threshold value becomes the filter. This contour and its interior can be thought of as the
10 union of many small rectangular regions ("tiles"), each of which is bracketed by low and high cutoff values for each of the parameters.

The predictions of different algorithm versions can also be combined by forming the intersection of two or more different predictions. The reliability of predictions within such intersection sets is enhanced because such sets are, by
15 definition, insensitive to changes in the details of the predictive algorithm. Intersection is a useful method for reducing the number of predicted probes when a single algorithm version produces too many candidate probes for efficient experimental evaluation.

The most specific oligonucleotide probe set (i.e., the set least likely to
20 include poor probes) will be the intersection set from multiple algorithms. Clusters that have overlapping oligonucleotide probes from multiple algorithms constitute the intersection set of oligonucleotide probes. The oligonucleotide probe that is in the center of an intersection cluster is chosen. This central oligonucleotide probe may have the highest probability of predicting a peak or, in other words, of binding
25 well to the target nucleotide sequence. Oligonucleotide probes on either side of center, which are still within the intersection cluster, may also be selected. The distance of these "side" oligonucleotide probes from the center generally will be shorter or longer depending upon the length of the cluster.

The most sensitive set of oligonucleotide probes (i.e., the set most likely to
30 include at least one good probe) is generally the union set from multiple algorithms. Clusters that are predicted by at least one type of algorithm constitute the union set of oligonucleotide probes. The oligonucleotide probe in the center of a union cluster is chosen. Oligonucleotide probes on either side of center, which

are still within the union cluster, usually are also chosen. The distance of these side probes from the center will be shorter or longer depending upon the length of the cluster. In summary, the combination of using the stability subsequence parameter, tiling multiple filter sets, and making union and intersection cluster sets of oligonucleotide probes exhibits very high sensitivity and specificity in predicting oligonucleotide probes that effectively hybridize to a target nucleotide sequence of interest.

Another aspect of the present invention is a computer based method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides within a nucleotide sequence that is hybridizable with the target nucleotide sequence is identified under computer control. The oligonucleotides are chosen to sample the entire length of the nucleotide sequence. A value is determined and evaluated under computer control for each of the oligonucleotides for at least one parameter that is independently predictive of the ability of each of the oligonucleotides to hybridize to the target nucleotide sequence. The parameter values are stored. Based on the examination of the stored parameter values, a subset of oligonucleotides within the predetermined number of unique oligonucleotides is identified under computer control. Then, oligonucleotides in the subset that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence are identified under computer control.

A computer program is utilized to carry out the above method steps. The computer program provides for input of a target-hybridizable or target-complementary nucleotide sequence, efficient algorithms for computation of oligonucleotide sequences and their associated predictive parameters, efficient, versatile mechanisms for filtering sets of oligonucleotide sequences based on parameter values, mechanisms for computation of the size of clusters of oligonucleotide sequences that pass multiple filters, and mechanisms for outputting the final predictions of the method of the present invention in a versatile, machine-readable or human-readable form.

Another aspect of the present invention is a computer system for conducting a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. An input means for introducing a target

nucleotide sequence into the computer system is provided. The input means may permit manual input of the target nucleotide sequence. The input means may also be a database or a standard format file such as GenBank. Also included in the system is means for determining a number of unique oligonucleotide sequences
5 that are within a nucleotide sequence that is hybridizable with the target nucleotide sequence. The oligonucleotide sequences is chosen to sample the entire length of the nucleotide sequence. Suitable means is a computer program or software, which also provides memory means for storing the oligonucleotide sequences. The system also includes means for controlling the computer system
10 to carry out a determination and evaluation for each of the oligonucleotide sequences a value for at least one parameter that is independently predictive of the ability of each of the oligonucleotide sequences to hybridize to the target nucleotide sequence. Suitable means is a computer program or software such as, for example, Microsoft® Excel spreadsheet, Microsoft® Access relational
15 database or the like, which also provides memory means for storing the parameter values. The system further comprises means for controlling the computer to carry out an identification of a subset of oligonucleotide sequences within the number of unique oligonucleotide sequences based on the automated examination of the stored parameter values. Suitable means is a computer program or software,
20 which also allocates memory means for storing the subset of oligonucleotides. The system also includes means for controlling the computer to carry out an identification of oligonucleotide sequences in the subset that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence. Suitable means is a computer program or software, which also
25 allocates memory means for storing the oligonucleotide sequences in the subset. The computer system also includes means for outputting data relating to the oligonucleotide sequences in the subset. Such means may be machine readable or human readable and may be software that communicates with a printer, electronic mail, another computer program, and the like. One particularly
30 attractive feature of the present invention is that the outputting means may communicate directly with software that is part of an oligonucleotide synthesizer. In this way the results of the method of the present invention may be used directly to provide instruction for the synthesis of the desired oligonucleotides.

Another advantage of the present invention is that it may be used to predict efficient hybridization oligonucleotides for each of multiple target sequences. Thus, very large arrays may be constructed and tested with minimal synthesis of oligonucleotides.

5

EXAMPLES

The invention is demonstrated further by the following illustrative examples. Parts and percentages are by weight unless otherwise indicated. Temperatures are in degrees Centigrade (°C) unless otherwise specified. The following preparations and examples illustrate the invention but are not intended to limit its scope. All reagents used herein were from Amresco, Inc., Solon, Ohio (buffers), Pharmacia Biotech, Piscataway, N.J. (nucleoside triphosphates) or Promega, Madison, Wisconsin (RNA polymerases) unless indicated otherwise.

10

15

Example 1

Synopsis: Data from labeled RNA target hybridizations to surface-bound DNA probes directed against 4 different gene sequences were compared to the predictions of the preferred version of the prediction algorithm illustrated by the flow chart in Fig. 2. The RNA targets were sequences derived from the human immunodeficiency virus protease-reverse transcriptase region (HIV PRT; sense-strand target polynucleotide), human glyceraldehyde-3-phosphate dehydrogenase gene (G3PDH; antisense-strand target polynucleotide), human tumor suppressor p53 gene (p53; antisense-strand target polynucleotide) and rabbit β -globin gene (β -globin; antisense-strand target polynucleotide). The GenBank accession numbers for the gene sequences, number of data points collected and temperature of hybridization have all been previously listed in Table 2.

20

25

Materials and Methods: Three different experimental systems and two different labeling schemes were used to collect data.

30

The sequence and hybridization data for β -globin were taken from the literature (see Milner *et al.*, (1997), *supra*; in this experiment, ^{32}P -radiolabeled RNA target was used.

The hybridization data for HIV PRT were obtained using an Affymetrix GeneChip™ HIV PRT-sense probe array (i.e. sense strand target polynucleotide) (GeneChip™ HIV PRT 440s, Affymetrix Corporation, Santa Clara, California) as specified by the manufacturer, except that the fluorescein-labeled RNA target was not fragmented prior to hybridization and that hybridization was performed for 24 hours. The concentration of fluorescein-labeled RNA used was 26.3 nM; label density was approximately 18 fluoresceinated uridyl nucleotides per 1 kilobase (kb) RNA transcript. The raw data were collected by scanning the array with a GeneChip™ Scanner 50 (Affymetrix Corporation, Santa Clara, California), as specified by the manufacturer. The raw data were reduced to a feature-averaged (".CEL") file, using the GeneChip™ software supplied with the scanner. Finally, a table of hybridization intensities for perfect-complement 20-mer probes was constructed using the ASCII feature map file supplied with the GeneChip™ software to connect probe sequences to measured hybridization intensities. The resulting data set contained data for every overlapping 20-mer probe to the target sequence.

The data for G3PDH and p53 were measured using 93-feature arrays constructed using commercially available streptavidin-coated microtiter plates (Pierce Chemical Company, Rockford, IL). Every tenth possible 25-mer probe complementary to each target was synthesized and 3'-biotinylated by a contract synthesis vendor (Operon, Inc., Alameda, CA). The 3'-linked biotin was used to anchor individual probes to microtiter wells, via the well known, strong affinity of streptavidin for biotin. Biotinylated DNA probes were resuspended to a concentration of 10 μM in hybridization buffer (5x sodium chloride-sodium phosphate-disodium ethylenediaminetetraacetate (SSPE), 0.05% Triton X-100, filter-sterilized; 1x SSPE is 150 mM sodium chloride, 10 mM sodium phosphate, 1 mM disodium ethylenediaminetetraacetate (EDTA), pH 7.4). Individual probes were diluted 1:10 in hybridization buffer into specified wells (100 μl total volume per well) of a streptavidin-coated microtiter plate; probes were allowed to bind to the covered plates overnight at 35°C. The other 3 wells of the 96-well microtiter

plate were probe-less controls. The coated plates were washed with 3 x 200 µl of wash buffer (6x SSPE, 0.005% Triton X-100, filter-sterilized). Fluorescein-labeled RNA (100 µl of a 10 nM solution in hybridization buffer) was added to each well. The plates were covered and hybridized at 35°C for 20-24 hours. The hybridized
5 plates were washed with 3 x 200 µl of wash buffer. Label was then released in each well by adding 100 µl of 20 µg/ml RNAase I (Sigma Chemical Company, St. Louis, MO) in Tris-EDTA (TE) (10 mM Tris(hydroxymethyl)aminomethane (Tris), 1 mM EDTA, pH 8.0, sterile) and incubating at 35°C for at least 30 minutes. The fluorescence released from the surface of each well was quantitated with a
10 PerSeptive Biosystems Cytofluor II microtiter plate fluorimeter (PerSeptive Biosystems, Inc., Framingham, MA) using the manufacturer's recommended excitation and emission filter sets for fluorescein. Each plate hybridization was performed in quadruplicate, and the data for each probe were averaged to obtain the hybridization intensity.

15 Labeled RNA targets specific for G3PDH and p53 were produced via T7 RNA polymerase transcription of DNA templates in the presence of fluorescein-UTP (Boehringer Mannheim Corporation, Indianapolis, IN), using the same method as that outlined by Affymetrix for their GeneChip™ HIV PRT sense probe array. The DNA template for G3PDH was purchased from a commercial source
20 (Clontech, Inc., Palo Alto, CA). The DNA template for p53 was obtained by sub-cloning a PCR fragment from an ATCC-derived reference clone (No. 57254) of human p53 into the commercially-available PCR cloning vector pCR2.1-TOPO (Invitrogen, Inc., Carlsbad, CA), then linearizing the plasmid at the end of the polycloning site opposite the vector-derived T7 promoter.

25 Probe predictions were performed using a software application (referred to as "p5") that was built atop Microsoft's Access relational database application, using added Visual Basic modules, the TrueDB Grid Pro 5.0 (Apex Software Corporation, Pittsburgh, PA) enhancement to Visual Basic, and a version of the FORTRAN application MFOLD, modified to run in a Windows NT 4.0 environment,
30 as an ActiveX control. The Visual Basic source code for the p5 software application is found in the Microfiche appendix to this specification. The DNA target sequence complements that were input into p5 for division into potential oligonucleotide probe sequences are listed below:

Parent Sequence Accession No.: K03256

Locus: BUNGLOB.DNA (portion of rabbit β -globin)

Length: 122

5 1 TTCTTCCACA TTCACCTTGC CCCACAGGGC AGTGACCGCA GACTTCTCCT CACTGGACAG
 61 ATGCACCATT CTGTCTGTTT TGGGGGATTG CAAGTAAACA CAGTTGTGTC AAAAGCAAGT
 121 GT SEQ ID NO:36

10 Parent Sequence Accession No.: M15654

Locus: HIV_PRTA.S (HIV PRT antisense; parses into probes specific for sense-strand target)

Length: 1040

15 1 TGTACTGTCC ATTTATCAGG ATGGAGTTCA TAACCCATCC AAAGGAATGG AGGTTCTTTC
 61 TGATGTTTTT TGTCTGGTGT GGTAAGTCCC CACCTCAACA GATGTTGTCT CAGCTCCTCT
 121 ATTTTTGTTC TATGCTGCCC TATTTCTAAG TCAGATCCTA CATACAAATC ATCCATGTAT
 181 TGATAGATAA CTATGTCTGG ATTTTGTTTT TTAAGAGGCT CTAAGATTTT TGTGATGCTA
 241 CTTTGGATAA TTGCTGGTGA TCCTTTCCAT CCCTGTGGAA GCACATTGTA CTGATATCTA
 301 ATCCCTGGTG TCTCATTGTT TATACTAGGT ATGGTAAATG CAGTATACTT CCTGAAGTCT
20 361 TCATCTAAGG GAACTGAAAA ATATGCATCA CCCACATCCA GTACTGTTAC TGATTTTTTTC
 421 TTTTTTAACC CTGCGGGATG TGGTATTCCCT AATTGAACTT CCCAGAAGTC TTGAGTTCTC
 481 TTATTAAGTT CTCTGAAATC TACTAATTTT CTCCATTTAG TACTGTCTTT TTTCTTTATG
 541 GCAAATACTG GAGTATTGTA TGGATTCTCA GGCCCAATTT TTGAAATTTT CCCTTCCTTT
 601 TCCATTTCTG TACAAATTTT TACTAATGCT TTTATTTTTT CTTCTGTCAA TGGCCATTGT
25 661 TTAACTTTTG GGCCATCCAT TCCTGGCTTT AATTTTACTG GTACAGTCTC AATAGGGCTA
 721 ATGGGAAAAT TTAAAGTGCA ACCAATCTGA GTCAACAGAT TTCTTCCAAT TATGTTGACA
 781 GGTGTAGGTC CTACTAATAC TGTACCTATA GCTTTATGTC CACAGATTTT TATGAGTATC
 841 TGATCATACT GTCTTACTTT GATAAAACCT CCAATTCCCC CTATCATTTT TGGTTTCCAT
 901 CTTCTGGGCA AACTCATTTT TTCTAATACT GTATCATCTG CTCCTGTATC TAATAGAGCT
30 961 TCCTTTAGTT GCCCCCTAT CTTTATTGTG ACGAGGGGTC GTTGCCAAAG AGTGATCTGA
 1021 GGGAAGTTAA AGGATACAGT SEQ ID NO:37

Parent Sequence Accession No.: X01677

35 Locus: G3PDH (Clontech G3PDH template - parses into probes specific for antisense-strand target)

Length: 999

40 1 GAAGGTCGGA GTCAACGGAT TTGGTCGTAT TGGGCGCCTG GTCACCAGGG CTGCTTTTAA
 61 CTCTGGTAAA GTGGATATTG TTGCCATCAA TGACCCCTTC ATTGACCTCA ACTACATGGT
 121 TTACATGTTT CAATATGATT CCACCCATGG CAAATTCCAT GGCACCGTCA AGGCTGAGAA
 181 CGGGAAGCTT GTCATCAATG GAAATCCCAT CACCATCTTC CAGGAGCGAG ATCCCTCCAA
 241 AATCAAGTGG GGCGATGCTG GCGCTGAGTA CGTCGTGGAG TCCACTGGCG TCTTACCAC
45 301 CATGGAGAAG GCTGGGGCTC ATTTGCAGGG GGGAGCCAAA AGGGTCATCA TCTCTGCCCC
 361 CTCTGCTGAT GCCCCATGT TCGTCATGGG TGTGAACCAT GAGAAGTATG ACAACAGCCT
 421 CAAGATCATC AGCAATGCCT CCTGCACCAC CAACTGCTTA GCACCCCTGG CCAAGGTCAT
 481 CCATGACAAC TTTGGTATCG TGGGAAGGACT CATGACCACA GTCCATGCCA TCACTGCCAC
 541 CCAGAAGACT GTGGATGGCC CCTCCGGGAA ACTGTGGCGT GATGGCCGCG GGGCTCTCCA
 601 GAACATCATC CTTGCCTCTA CTGGCGCTGC CAAGGCTGTG GGCAAGGTCA TCCCTGAGCT
50 661 AGACGGGAAG CTCACCTGGCA TGGCCTTCCG TGTCCCCACT GCCAACGTGT CAGTGGTGGA
 721 CCTGACCTGC CGTCTAGAAA AACCTGCCAA ATATGATGAC ATCAAGAAGG TGGTGAAGCA
 781 GGCCTCGGAG GGCCCCCTCA AAGGCATCCT GGCGTACACT GAGCACCAGG TGGTCTCCTC
 841 TGAATTCAAC AGCGACACCC ACTCCTCCAC CTTTGACGCT GGGGCTGGCA TTGCCCTCAA
 901 CGACCACTTT GTCAAGCTCA TTTCTGGTGA TGACAACGAA TTTGGCTACA GCAACAGGGT
55 961 GGTGGACCTC ATGGCCCACA TGCTATAGTG AGTCGTATT SEQ ID NO:38

Parent Sequence Accession No.: X54156

Locus: HSP53PCRa (p53 template - parses into probes specific for antisense-strand target)

Length: 1049

5
1 GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA GACCGGCGCA CAGAGGAAGA GAATCTCCGC
61 AAGAAAGGGG AGCCTCACCA CGAGCTGCCC CCAGGGAGCA CTAAGCGAGC ACTGCCCCAAC
121 AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACCACTGG ATGGAGAATA TTTACCCCTT
181 CAGATCCGTG GGCGTGAGCG CTTCGAGATG TTCCGAGAGC TGAATGAGGC CTTGGAATC
10 241 AAGGATGCCC AGGCTGGGAA GGAGCCAGGG GGGAGCAGGG CTCCTCCAG CCACCTGAAG
301 TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT AAAAACTCA TGTTCAAGAC AGAAGGGCCT
361 GACTCAGACT GACATTCTCC ACTTCTTGTT CCCCCTGAC AGCCTCCCTC CCCCATCTCT
421 CCCTCCCCTG CCATTTTGGG TTTTGGGTCT TTGAACCCCTT GCTTGCAATA GGTGTGCGTC
481 AGAAGCACCC AGGACTTCCA TTTGCTTTGT CCCGGGGCTC CACTGAACAA GTTGGCCTGC
15 541 ACTGGTGTTT TGTTGTGGGG AGGAGGATGG GGAGTAGGAC ATACCAGCTT AGATTTTAAG
601 GTTTTTACTG TGAGGGATGT TTGGGAGATG TAAGAAATGT TCTTGCAGTT AAGGGTTAGT
661 TTACAATCAG CCACATTCTA GGTAAGTAGG GGCCCACTTC ACCGTACTAA CCAGGGAAGC
721 TGTCCCTCAT GTTGAATTTT CTCTAACTTC AAGGCCCATATA TCTGTGAAAT GCTGGCATT
781 GCACCTACCT CACAGAGTGC ATTGTGAGGG TTAATGAAAT AATGTACATC TGGCCTTGAA
20 841 ACCACCTTTT ATTACATGGG GTCTAAACT TGACCCCTT GAGGGTGCCT GTTCCCTCTC
901 CCTCTCCCTG TTGGCTGGTG GGTTGGTAGT TTCTACAGTT GGGCAGCTGG TTAGGTAGAG
961 GGAGTTGTCA AGTCTTGCTG GCCCAGCCAA ACCCTGTCTG ACAACCTCTT GGTGACCTT
1021 AGTACCTAAA AGGAAATCTC ACCCCATCC SEQ ID NO:39

25 The sequences indicated above, which are complements of the target sequences, were divided into overlapping oligonucleotide sequences with one nucleotide between starting positions. The oligonucleotide sequence lengths were 17 (rabbit β -globin), 20 (HIV PRT) or 25 (G3PDH; p53). The oligonucleotide sequence lengths were dictated by the probe lengths used in the experiments to
30 which the predictions were compared. The RNA target concentrations used to calculate predicted RNA/DNA duplex melting temperatures were 100 pM (rabbit β -globin), 26.3 nM (HIV PRT) and 10 nM (G3PDH; p53). These were also dictated by experimental conditions for the comparison data. The cut-off filter used for the predicted free energy of the most stable probe sequence intramolecular structure,

35 ΔG_{MFOLD} , was

$$\Delta G_{MFOLD} \geq -0.4 \frac{\text{kcal}}{\text{mole}}.$$

The filter condition used for the predicted RNA/DNA duplex melting temperature was

40
$$25^{\circ}\text{C} \leq T_m + 16.6 \log([Na^+]) - T_{hyb} \leq 50^{\circ}\text{C},$$

where T_m is the target concentration-dependent value of the predicted RNA/DNA duplex melting temperature before correction for salt concentration, the term " $16.6 \log([Na^+])$ " corrects the melting temperature for salt effects, and T_{hyb} is the hybridization temperature. The values of the salt correction term and T_{hyb} have
5 already been listed in Table 2. For convenient use within p5, the above condition was algebraically rearranged into the equivalent form

$$25^{\circ}C - 16.6 \log([Na^+]) + T_{hyb} \leq T_m \leq 50^{\circ}C - 16.6 \log([Na^+]) + T_{hyb}.$$

Clusters were ranked according to the number of contiguous oligonucleotide
10 sequences that passed through the filter set ("contig" length).

Results: The detailed analysis results for rabbit β -globin are presented in Table 3; a graphical summary of the results is shown in Fig. 4. In Table 3, values of T_m and ΔG_{MFOLD} that were excluded by the filter set are shown with a line through
15 them, and table entries for contig length are shown in gray when the oligonucleotide sequence in question was not in a contig. The top 20% of the observed hybridization intensities are shown underlined.

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Table 3

Position	Oligonucleotide Sequence	SEQ ID NO:	T _m (°C)	ΔG _{MFOLD} (kcal/mole)	Contig Length	Hybridization Intensity (Milner <i>et al.</i> , 1997)
1	TTCTTCCACATTACCT	40	53.62	5.00		100
2	TCTTCCACATTACCTT	41	53.62	5.00		130
3	CTTCCACATTACCTTG	42	52.19	0.90		130
4	TTCCACATTACCTTGC	43	54.50	0.50		200
5	TCCACATTACCTTGCC	44	58.46	0.50	7	120
6	CCACATTACCTTGCCC	45	61.10	0.50	7	180
7	CACATTACCTTGCCCC	46	61.10	0.50	7	<u>230</u>
8	ACATTACCTTGCCCCA	47	61.10	0.50	7	<u>220</u>
9	CATTACCTTGCCCCAC	48	61.10	0.90	7	<u>320</u>
10	ATTACCTTGCCCCACA	49	61.10	0.70	7	<u>310</u>
11	TCACCTTGCCCCACAG	50	61.33	0.50	7	<u>320</u>
12	TCACCTTGCCCCACAGG	51	63.70	-0.60		<u>390</u>
13	CACCTTGCCCCACAGGG	52	64.85	-1.60		<u>410</u>
14	ACCTTGCCCCACAGGGC	53	68.01	-4.10		<u>240</u>
15	CCTTGCCCCACAGGGCA	54	68.63	-5.40		50
16	CTTGCCCCACAGGGCAG	55	64.95	-5.60		20
17	TTGCCCCACAGGGCAGT	56	66.31	-5.60		20
18	TGCCCCACAGGGCAGTG	57	65.79	-5.40		20
19	GCCCCACAGGGCAGTGA	58	67.37	-4.10		20
20	CCCCACAGGGCAGTGAC	59	63.42	-1.60		40
21	CCCACAGGGCAGTGACC	60	63.42	-1.40		20
22	CCACAGGGCAGTGACCG	61	59.85	-1.40		20
23	CACAGGGCAGTGACCGC	62	60.14	-1.00		20
24	ACAGGGCAGTGACCGCA	63	60.14	-0.50		20
25	CAGGGCAGTGACCGCAG	64	59.76	-0.50		30
26	AGGGCAGTGACCGCAGA	65	59.83	-0.50		20
27	GGGCAGTGACCGCAGAC	66	60.22	-0.50		30
28	GGCAGTGACCGCAGACT	67	59.53	-0.50		30
29	GCAGTGACCGCAGACTT	68	57.06	-0.40		30
30	CAGTGACCGCAGACTTC	69	53.99	-0.40		40
31	AGTGACCGCAGACTTCT	70	54.74	-0.20		40
32	GTGACCGCAGACTTCTC	71	55.99	0.60	7	100
33	TGACCGCAGACTTCTCC	72	57.01	0.60	7	120
34	GACCGCAGACTTCTCCT	73	59.22	0.60	7	180
35	ACCGCAGACTTCTCCTC	74	59.28	0.60	7	210
36	CCGCAGACTTCTCCTCA	75	60.07	0.60	7	200
37	CGCAGACTTCTCCTCAC	76	56.34	0.60	7	190
38	GCAGACTTCTCCTCACT	77	57.79	0.60	7	<u>240</u>
39	CAGACTTCTCCTCACTG	78	52.93	0.60		<u>240</u>
40	AGACTTCTCCTCACTGG	79	54.44	0.00		<u>340</u>

Table 3

Position	Oligonucleotide Sequence	SEQ ID NO:	T _m (°C)	ΔG _{MFOLD} (kcal/mole)	Contig Length	Hybridization Intensity (Milner <i>et al.</i> , 1997)
41	GACTTCTCCTCACTGGA	80	55.77	-1.40		340
42	ACTTCTCCTCACTGGAC	81	54.85	-1.60		240
43	CTTCTCCTCACTGGACA	82	55.75	-1.60		240
44	TTCTCCTCACTGGACAG	83	53.66	-1.60		120
45	TCTCCTCACTGGACAGA	84	54.82	-1.60		100
46	CTCCTCACTGGACAGAT	85	53.36	-1.60		110
47	TCCTCACTGGACAGATG	86	51.10	-1.40		80
48	CCTCACTGGACAGATGC	87	54.25	0.00		240
49	CTCACTGGACAGATGCA	88	51.26	0.20		90
50	TCACTGGACAGATGCAC	89	49.63	0.20		30
51	CACTGGACAGATGCACC	90	52.74	0.50		100
52	ACTGGACAGATGCACCA	91	52.74	-0.50		80
53	CTGGACAGATGCACCAT	92	52.18	-1.00		90
54	TGGACAGATGCACCATT	93	50.39	-0.80		80
55	GGACAGATGCACCATT	94	51.75	0.30		180
56	GACAGATGCACCATTCT	95	51.05	-0.10		220
57	ACAGATGCACCATTCTG	96	49.56	-1.80		120
58	CAGATGCACCATTCTGT	97	52.19	-2.10		120
59	AGATGCACCATTCTGTC	98	52.06	-0.10		250
60	GATGCACCATTCTGTCT	99	54.18	0.30		520
61	ATGCACCATTCTGTCTG	100	52.60	0.40		980
62	TGCACCATTCTGTCTGT	101	56.05	0.20	2	780
63	GCACCATTCTGTCTGTT	102	56.52	0.20	2	810
64	CACCATTCTGTCTGTTT	103	52.06	0.20		220
65	ACCATTCTGTCTGTTTT	104	50.83	0.20		120
66	CCATTCTGTCTGTTTTG	105	50.18	0.20		120
67	CATTCTGTCTGTTTTGG	106	48.42	0.60		160
68	ATTCTGTCTGTTTTGGG	107	49.94	1.70		310
69	TTCTGTCTGTTTTGGGG	108	53.10	1.70		250
70	TCTGTCTGTTTTGGGGG	109	55.90	1.70	2	80
71	CTGTCTGTTTTGGGGGA	110	55.91	1.40	2	30
72	TGTCTGTTTTGGGGGAT	111	53.55	0.90		50
73	GTCTGTTTTGGGGGATT	112	54.00	0.90		10
74	TCTGTTTTGGGGGATTG	113	50.50	1.10		10
75	CTGTTTTGGGGGATTGC	114	53.77	2.20		10
76	TGTTTTGGGGGATTGCA	115	53.04	1.20		10
77	GTTTTGGGGGATTGCAA	116	51.04	0.00		5
78	TTTTGGGGGATTGCAAG	117	47.99	-0.20		5
79	TTTGGGGGATTGCAAGT	118	50.80	-0.20		5
80	TTGGGGGATTGCAAGTA	119	49.80	0.00		5

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Table 3

Position	Oligonucleotide Sequence	SEQ ID NO:	T _m (°C)	ΔG _{MFOLD} (kcal/mole)	Contig Length	Hybridization Intensity (Milner <i>et al.</i> , 1997)
81	TGGGGGATTGCAAGTAA	120	47.55	1.20		5
82	GGGGGATTGCAAGTAAA	121	45.76	1.40		5
83	GGGGATTGCAAGTAAAC	122	43.54	1.40		5
84	GGGATTGCAAGTAAACA	123	42.32	1.30		5
85	GGATTGCAAGTAAACAC	124	40.11	0.90		5
86	GATTGCAAGTAAACACA	125	38.94	0.50		5
87	ATTGCAAGTAAACACAG	126	37.61	0.50		5
88	TTGCAAGTAAACACAGT	127	40.35	0.50		5
89	TGCAAGTAAACACAGTT	128	40.35	0.30		5
90	GCAAGTAAACACAGTTG	129	40.35	0.10		10
91	CAAGTAAACACAGTTGT	130	38.98	-0.30		5
92	AAGTAAACACAGTTGTG	131	37.40	-0.90		5
93	AGTAAACACAGTTGTGT	132	42.02	-2.30		5
94	GTAAACACAGTTGTGTGTC	133	43.15	-2.50		5
95	TAAACACAGTTGTGTCA	134	41.73	-2.50		5
96	AAACACAGTTGTGTCAA	135	40.67	-2.50		5
97	AACACAGTTGTGTCAAA	136	40.67	-2.50		5
98	ACACAGTTGTGTCAAAA	137	40.67	-2.30		10
99	CACAGTTGTGTCAAAAG	138	40.20	-1.20		15
100	ACAGTTGTGTCAAAAGC	139	42.93	-0.50		30
101	CAGTTGTGTCAAAAGCA	140	43.99	0.20		25
102	AGTTGTGTCAAAAGCAA	141	40.67	-0.10		25
103	GTTGTGTCAAAAGCAAG	142	40.67	-0.30		20
104	TTGTGTCAAAAGCAAGT	143	40.67	-0.10		120
105	TGTGTCAAAAGCAAGTG	144	40.40	0.50		20

In Fig. 4, the hybridization intensity observed experimentally is plotted as a function of oligonucleotide starting position in the target-complementary sequence that was input into p5. The identified contigs are plotted as horizontal bars, with the contig rank (by length) shown in parentheses next to each bar. It is clear from Table 3 and Fig. 4 that the prediction algorithm identified contigs that overlap all of the "top 20%" hybridization intensity peaks observed. Iterative experimental improvement of these predictions would converge on each of the observed intensity maxima in 3-4 iterations.

Prediction worksheets for HIV PRT, G3PDH and p53 were prepared in a manner similar to that for rabbit β-globin as shown in Table 3, except that the probes were longer as indicated above and that approximately 1,000 probes were

analyzed for each of these genes. The results of these analyses are shown in Fig. 5 (HIV PRT), Fig. 6 (G3PDH) and Fig. 7 (p53). In Fig. 5, data are plotted for all possible 20-mer oligonucleotide probes. In Figs. 6 and 7, data were available for only every 10th 25-mer probe, and the actual data points are plotted as open diamonds.

It is clear from Figs. 5-7 that the hybridization efficiency prediction algorithm of the present invention performed well in the task of identifying regions with observed high hybridization intensity. In each case, the 4 longest contigs point to good-to-excellent regions for experimental investigation. It should be noted that the contigs usually bracket observed intensity peaks; experimental iterative refinement would therefore be expected to converge in 2-3 iterations. By this is meant that certain oligonucleotides from the identified contigs are prepared and subjected to evaluation in actual hybridization experiments. Based on the results of such experiments, the observed signal is evaluated to determine whether the oligonucleotides are hybridizing to the left of, the right of, or on the center of a peak with respect to the graphed data. The next iteration is carried out to experimentally evaluate the hybridization efficiency of probes that are inferred to lie closer to the peak of hybridization efficiency, based on the data from the previous iteration. Iteration is continued until the signal level is deemed acceptable by the user, or the local hybridization efficiency maximum is reached (i.e. the best probe in the cluster identified by the method of the current invention has been experimentally identified). A detailed illustration of this process is shown in Example 3.

It should be noted that clusters of predictions that overlap the maxima of observed peaks of hybridization efficiency will often yield user-acceptable probes on the first iteration. Thus, the method of the present invention is much more efficient than current methods in which every potential probe is synthesized. For instance, in the HIV PRT example shown in Fig. 5, at least 3 good probes would be identified after synthesis of ~10 test probes (i.e. statistical sampling of the 3 longest contigs). This is much more efficient than the ~1,000 probes represented by the data in Fig. 5.

Example 2

Synopsis: Data from a labeled RNA target hybridization to an Affymetrix GeneChip™ HIV PRT-sense probe array (GeneChip™ HIV PRT 440s, Affymetrix Corporation, Santa Clara, CA) were compared to the predictions of the window-averaged composite dimensionless score version of the method of the present invention.

Materials and Methods: Data were obtained as described for the Affymetrix GeneChip™ HIV PRT-sense probe array (GeneChip™ HIV PRT 440s, Affymetrix Corporation, Santa Clara, California) in Example 1. The DNA sequence (SEQ ID NO: 37) complementary to the fluorescein-labeled RNA target was divided into overlapping 20-mer oligonucleotide sequences spaced one nucleotide apart, using the prototype application p5; p5 was also used to calculate the predicted values of the RNA/DNA heteroduplex melting temperature (T_m) and the free energy of the most stable predicted probe intramolecular structure, ΔG_{MFOLD} , as described in Example 1. The probe sequences and parameter values were then transferred to a Microsoft Excel spreadsheet, which was used to complete the predictions of efficient and inefficient probes. The weight was obtained by optimizing the performance of the algorithm with the data of Milner *et al.*, *supra*, as the training data using the Microsoft® Excel® spreadsheet software. The composite score was calculated using a weight of 0.62 for the dimensionless T_m score and a weight of 0.38 for the ΔG_{MFOLD} dimensionless score. The windowed-averaging was performed using a window width of 7 and Microsoft® Excel® spreadsheet software. Finally, the oligonucleotide sequences having the top 10% of the window-averaged composite dimensionless scores were predicted to be efficient probes, while the oligonucleotide sequences having the bottom 10% of the window-averaged composite dimensionless scores were predicted to be inefficient probes.

Results: The calculated parameters and scores are shown in Table 4; the algorithm predictions are also shown diagrammatically in Figure 8. In Table 4, window-averaged composite score values that were in the top 10% of the

distribution of values are shown in bold type, values that were in the bottom 10% are shown in italics, and all other values are shown with a line through them. It is clear from both Table 4 and Figure 8 that the window-averaged composite dimensionless score embodiment of the current invention correctly predicted both efficient and inefficient hybridization probes for HIV PRT sense-strand RNA. As in Example 1, statistical sampling of contiguous stretches of predicted "good" probes would lead to convergence of the design process to the best probes in each region in 2-4 design iterations.

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
1	GTACTGTCCATTATCAGGA	145	64.16	-0.10	0.557	-0.199	0.269		1152.2
2	TACTGTCCATTATCAGGAT	146	60.91	-0.40	0.080	-0.460	-0.125		1040.7
3	ACTGTCCATTATCAGGATG	147	61.41	-0.90	0.152	-0.895	-0.246		291.9
4	CTGTCCATTATCAGGATGG	148	63.46	-0.90	0.453	-0.895	-0.059	-0.468	221.8
5	TGTCCATTATCAGGATGGA	149	62.82	-0.90	0.360	-0.895	-0.117	-0.284	148.3
6	GTCCATTATCAGGATGGAG	150	63.15	-1.90	0.408	-1.764	-0.418	-0.308	84.6
7	TCCATTATCAGGATGGAGT	151	63.15	-2.10	0.408	-1.938	-0.484	-0.252	128.7
8	CCATTATCAGGATGGAGTT	152	62.03	-1.90	0.245	-1.764	-0.519	-0.242	94.6
9	CAATTATCAGGATGGAGTTC	153	59.53	-0.60	-0.122	-0.634	-0.317	-0.236	157.5
10	ATTATCAGGATGGAGTTCA	154	59.53	0.80	-0.122	0.583	0.146	-0.227	316.9
11	TTATCAGGATGGAGTTTCAT	155	59.53	0.40	-0.122	0.236	0.014	-0.494	360.2
12	TTATCAGGATGGAGTTTCATA	156	58.58	0.40	-0.262	0.236	-0.073	-0.405	403.8
13	TATCAGGATGGAGTTTCATAA	157	56.21	0.20	-0.609	0.062	-0.354	-0.044	382.5
14	ATCAGGATGGAGTTTCATAAC	158	57.34	0.20	-0.444	0.062	-0.252	-0.004	324.4
15	TCAGGATGGAGTTTCATAACC	159	61.25	0.20	0.129	0.062	0.104	-0.035	320.5
16	CAGGATGGAGTTTCATAACCC	160	63.57	0.20	0.470	0.062	0.315	-0.401	238.9
17	AGGATGGAGTTTCATAACCCA	161	63.57	-0.10	0.470	-0.199	0.216	-0.457	202.3
18	GGATGGAGTTTCATAACCCAT	162	63.34	-1.30	0.436	-1.243	-0.202	-0.420	113.6
19	GATGGAGTTTCATAACCCATC	163	62.24	-2.00	0.275	-1.851	-0.533	-0.099	97.7
20	ATGGAGTTTCATAACCCATCC	164	64.62	-3.30	0.624	-2.982	-0.746	-0.400	143.3
21	TGGAGTTTCATAACCCATCCC	165	68.18	-2.00	1.146	-1.851	0.007	-0.409	484.6
22	GGAGTTTCATAACCCATCCCA	166	69.39	-1.60	1.324	-1.504	0.249	-0.058	857.6
23	GAGTTTCATAACCCATCCCAA	167	64.93	-0.20	0.670	-0.286	0.307	0.053	991.4
24	AGTTTCATAACCCATCCCAAA	168	61.82	0.20	0.213	0.062	0.155	0.473	907.0
25	GTTTCATAACCCATCCCAAG	169	61.82	0.20	0.213	0.062	0.155	0.437	887.9
26	TTTCATAACCCATCCCAAGG	170	61.36	0.60	0.145	0.410	0.246	0.053	1015.3

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
27	TCATAACCCATCCCAAAGGA	171	62.21	-0.10	0.270	-0.199	0.092	-0.040	279.7
28	CATAACCCATCCCAAAGGAA	172	59.26	-0.30	-0.163	-0.373	-0.243	-0.124	210.7
29	ATAACCCATCCCAAAGGAAT	173	58.19	-0.30	-0.320	-0.373	-0.340	-0.204	179.9
30	TAACCCATCCCAAAGGAATG	174	58.13	-0.30	-0.328	-0.373	-0.345	-0.309	91.8
31	AACCCATCCCAAAGGAATGG	175	60.78	-1.30	0.061	-1.243	-0.435	-0.412	44.6
32	ACCCATCCCAAAGGAATGGA	176	63.69	-2.00	0.487	-1.851	-0.401	-0.488	42.9
33	CCCATCCCAAAGGAATGGAG	177	63.40	-2.20	0.445	-2.025	-0.494	-0.542	45.0
34	CCATCCCAAAGGAATGGAGG	178	62.34	-2.30	0.290	-2.112	-0.623	-0.579	45.3
35	CATCCCAAAGGAATGGAGGT	179	61.72	-2.60	0.199	-2.373	-0.778	-0.587	47.9
36	ATCCCAAAGGAATGGAGTT	180	60.90	-2.20	0.079	-2.025	-0.721	-0.580	49.2
37	TCCCAAAGGAATGGAGTTC	181	62.24	-2.20	0.274	-2.025	-0.600	-0.585	74.2
38	CCCAAAGGAATGGAGTTCT	182	62.71	-2.00	0.344	-1.851	-0.490	-0.572	125.5
39	CCAAAGGAATGGAGTTCTT	183	59.47	-0.70	-0.132	-0.721	-0.356	-0.485	183.3
40	CAAAGGAATGGAGTTCTTT	184	56.10	-0.30	-0.627	-0.373	-0.530	-0.380	261.4
41	AAAGGAATGGAGTTCTTTC	185	56.11	-0.30	-0.625	-0.373	-0.529	-0.277	518.3
42	AAGGAATGGAGTTCTTTCT	186	60.05	-0.30	-0.046	-0.373	-0.170	-0.206	716.5
43	AGGAATGGAGTTCTTTCTG	187	62.09	-0.30	0.253	-0.373	0.015	-0.164	1056.0
44	GGAATGGAGTTCTTTCTGA	188	63.23	-0.30	0.420	-0.373	0.119	-0.025	1084.3
45	GAATGGAGTTCTTTCTGAT	189	60.56	0.10	0.028	-0.025	0.008	0.119	1241.1
46	AATGGAGTTCTTTCTGATG	190	59.12	0.30	-0.183	0.149	-0.057	0.217	1278.8
47	ATGGAGTTCTTTCTGATGT	191	64.58	0.30	0.618	0.149	0.440	0.258	1616.0
48	TGGAGTTCTTTCTGATGTT	192	64.98	0.30	0.677	0.149	0.476	0.270	1677.5
49	GGAGTTCTTTCTGATGTTT	193	65.49	0.30	0.751	0.149	0.522	0.309	1963.1
50	GAGTTCTTTCTGATGTTTT	194	63.04	0.30	0.392	0.149	0.300	0.301	2126.1
51	AGTTCTTTCTGATGTTTTT	195	61.97	0.30	0.235	0.149	0.202	0.234	2143.3
52	GGTTCTTTCTGATGTTTTTT	196	62.11	0.30	0.256	0.149	0.215	0.180	3540.6
53	GTCTTTCTGATGTTTTTTTG	197	59.21	0.30	-0.170	0.149	-0.049	0.164	1728.7

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
54	TTCTTCTGATGTTTTTGT	198	59.21	0.30	-0.170	0.149	-0.049	0.454	1364.3
55	TCTTCTGATGTTTTTGT	199	60.35	0.50	-0.002	0.323	0.121	0.483	1788.4
56	CTTCTGATGTTTTTGTCT	200	60.96	1.20	0.086	0.931	0.407	0.253	2670.9
57	TTTCTGATGTTTTTGTCTG	201	58.76	1.20	-0.235	0.931	0.208	0.338	3336.2
58	TTCTGATGTTTTTGTCTGG	202	61.17	1.20	0.118	0.931	0.427	0.440	6883.6
59	TCTGATGTTTTTGTCTGGT	203	64.20	1.20	0.562	0.931	0.702	0.537	10227.0
60	CTGATGTTTTTGTCTGGTG	204	62.51	1.20	0.315	0.931	0.549	0.625	10965.0
61	TGATGTTTTTGTCTGGTGT	205	63.80	1.20	0.504	0.931	0.666	0.778	11133.0
62	GATGTTTTTGTCTGGTG	206	63.80	1.60	0.504	1.279	0.798	0.894	11503.0
63	ATGTTTTTGTCTGGTG	207	65.18	1.90	0.705	1.540	1.023	0.894	9492.8
64	TGTTTTTGTCTGGTG	208	68.78	1.70	1.234	1.366	1.284	0.914	10704.0
65	GTTTTTTGTCTGGTG	209	68.28	1.70	1.161	1.366	1.239	0.933	10741.0
66	TTTTTGTCTGGTG	210	62.37	1.70	0.294	1.366	0.701	0.950	9187.5
67	TTTTTGTCTGGTGTAAG	211	62.23	1.70	0.273	1.366	0.689	0.941	7871.0
68	TTTTTGTCTGGTGTAAGT	212	65.28	1.20	0.721	0.931	0.801	0.921	7209.1
69	TTTGTCTGGTGTAAGTC	213	66.56	1.20	0.908	0.931	0.917	0.959	8052.3
70	TTGTCTGGTGTAAGTCC	214	70.25	0.30	1.449	0.149	0.955	1.022	7230.6
71	TGCTGGTGTAAGTCCC	215	73.77	-0.10	1.966	-0.199	1.143	0.998	6809.5
72	GTCGTGGTGTAAGTCCC	216	77.74	-0.10	2.549	-0.199	1.504	0.913	7442.8
73	TCTGGTGTAAGTCCCCA	217	75.28	-0.50	2.187	-0.547	1.148	0.824	2627.7
74	CTGGTGTAAGTCCCCAC	218	74.18	-2.10	2.026	-1.938	0.519	0.784	1315.0
75	TGGTGTAAGTCCCCACC	219	75.80	-3.50	2.263	-3.156	0.204	0.680	4182.3
76	GGTGTAAGTCCCCACCT	220	77.89	-3.80	2.571	-3.417	0.296	0.548	474.7
77	GTGGTAAGTCCCCACCTC	221	77.05	-2.50	2.448	-2.286	0.649	0.429	682.4
78	TGTGGTAAGTCCCCACCTCA	222	74.71	-2.50	2.105	-2.286	0.436	0.465	679.1
79	TGTGGTAAGTCCCCACCTCAA	223	72.54	-2.10	1.785	-1.938	0.370	0.584	924.0
80	TGTAAGTCCCCACCTCAAC	224	69.94	-0.90	1.404	-0.895	0.531	0.667	835.5

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _M ^{FOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG _M ^{FOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
81	GGTAAGTCCCACTCAACA	225	71.14	-0.50	1.580	-0.547	0.772	0.687	1213.6
82	GTAAGTCCCACTCAACAG	226	68.97	0.90	1.262	0.670	1.037	0.763	1106.1
83	TAAGTCCCACTCAACAGA	227	67.18	0.90	0.999	0.670	0.874	0.872	1009.0
84	AAGTCCCACTCAACAGAT	228	67.68	0.50	1.073	0.323	0.788	0.908	1656.2
85	AGTCCCACTCAACAGATG	229	69.68	0.50	1.366	0.323	0.970	0.834	2178.3
86	GTCCTCCCACTCAACAGATG	230	72.56	0.20	1.789	0.062	1.132	0.679	2567.0
87	TCCCTCCCACTCAACAGATG	231	69.77	-0.10	1.379	-0.199	0.779	0.522	3000.5
88	CCCCACCTCAACAGATGTTG	232	68.19	-1.30	1.148	-1.243	0.240	0.354	2025.4
89	CCACCTCAACAGATGTTGT	233	67.78	-2.00	1.087	-1.851	-0.030	0.464	429.2
90	CCACCTCAACAGATGTTGTC	234	65.65	-2.00	0.775	-1.851	-0.223	-0.044	157.9
91	CACCTCAACAGATGTTGTC	235	63.85	-2.00	0.511	-1.851	-0.387	-0.244	135.3
92	ACCTCAACAGATGTTGTC	236	64.11	-2.00	0.549	-1.851	-0.363	-0.339	330.8
93	CCTCAACAGATGTTGTC	237	64.77	-2.00	0.646	-1.851	-0.303	-0.370	900.0
94	CTCAACAGATGTTGTC	238	61.08	-2.00	0.104	-1.851	-0.639	-0.300	1177.0
95	TCAACAGATGTTGTC	239	63.40	-2.00	0.444	-1.851	-0.428	-0.117	795.1
96	CAACAGATGTTGTC	240	63.91	-1.60	0.520	-1.504	-0.249	0.084	889.2
97	AACAGATGTTGTC	241	64.19	-0.10	0.560	-0.199	0.272	0.287	1703.6
98	ACAGATGTTGTC	242	70.61	0.00	1.503	-0.112	0.889	0.598	3115.2
99	CAGATGTTGTC	243	72.08	0.00	1.719	-0.112	1.023	0.847	4445.0
100	AGATGTTGTC	244	72.66	0.20	1.803	0.062	1.141	1.070	6762.8
101	GATGTTGTC	245	74.49	0.90	2.071	0.670	1.539	1.227	8845.0
102	ATGTTGTC	246	72.38	0.80	1.763	0.583	1.314	1.253	9010.6
103	TGTTGTC	247	72.38	0.80	1.763	0.583	1.314	1.260	19941.0
104	GTTGTC	248	72.97	0.80	1.849	0.583	1.368	1.257	12577.0
105	TTGTC	249	69.70	0.80	1.369	0.583	1.071	1.149	7503.3
106	TGTC	250	69.70	0.80	1.369	0.583	1.071	1.098	7033.8
107	GTCTCAGTCCTCTATTTT	251	70.26	0.80	1.451	0.583	1.121	1.024	8276.7

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _{Mfold} (kcal/mole @ 35 °C)	T _m Score	ΔG _{Mfold} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
108	TCTCAGCTCCTCTATTTTGG	252	66.57	0.80	0.910	0.583	0.786	0.942	2899.0
109	CTCAGCTCCTCTATTTTGT	253	68.39	0.80	1.177	0.583	0.952	0.923	2935.0
110	TCAGCTCCTCTATTTTGT	254	66.69	0.80	0.927	0.583	0.796	0.930	1512.8
111	CAGCTCCTCTATTTTGTTC	255	66.69	0.80	0.927	0.583	0.796	0.872	1708.8
112	AGCTCCTCTATTTTGTTC	256	67.52	1.00	1.050	0.757	0.939	0.833	1977.3
113	GCTCCTCTATTTTGTTC	257	66.63	1.80	0.919	1.453	1.122	0.809	2114.8
114	CTCCTCTATTTTGTTC	258	62.13	1.80	0.259	1.453	0.713	0.766	1527.3
115	TCCTCTATTTTGTTC	259	59.97	1.80	-0.058	1.453	0.516	0.695	1536.8
116	CCCTCTATTTTGTTC	260	62.84	1.80	0.363	1.453	0.777	0.642	1824.5
117	CTCTATTTTGTTC	261	60.87	1.50	0.074	1.192	0.499	0.588	1169.2
118	TCATTTTGTTC	262	58.71	1.50	-0.244	1.192	0.302	0.649	683.7
119	CTATTTTGTTC	263	61.60	1.50	0.181	1.192	0.565	0.765	1306.8
120	TATTTTGTTC	264	63.53	1.50	0.464	1.192	0.741	0.834	2523.6
121	ATTTTGTTC	265	67.96	1.50	1.113	1.192	1.143	0.931	6682.0
122	TTTGTTC	266	69.96	1.50	1.407	1.192	1.325	1.060	9417.4
123	TTTGTTC	267	69.01	1.50	1.267	1.192	1.239	1.151	10339.0
124	TTTGTTC	268	68.62	1.50	1.210	1.192	1.203	1.254	10750.0
125	TTTGTTC	269	68.62	1.50	1.210	1.192	1.203	1.282	11180.0
126	TTTGTTC	270	68.62	1.50	1.210	1.192	1.203	1.271	11060.0
127	TTTGTTC	271	70.37	1.80	1.468	1.453	1.462	1.221	16074.0
128	TTTGTTC	272	69.00	1.80	1.266	1.453	1.337	1.144	9183.8
129	TTTGTTC	273	68.05	1.80	1.127	1.453	1.251	1.082	8617.8
130	TTTGTTC	274	64.38	1.70	0.589	1.366	0.884	1.040	7286.8
131	TTTGTTC	275	62.71	1.50	0.344	1.192	0.666	0.978	3642.4
132	TTTGTTC	276	66.39	0.80	0.883	0.583	0.769	0.883	3799.7
133	TTTGTTC	277	67.95	0.80	1.112	0.583	0.911	0.749	3408.3
134	TTTGTTC	278	69.25	0.80	1.303	0.583	1.030	0.644	4017.4

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _{Mfold} (kcal/mole @ 35 °C)	T _m Score	ΔG _{Mfold} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
135	CTGCCCTATTCTAAGTCAG	279	65.26	0.80	0.718	0.583	0.667	0.536	2197.2
136	TGCCCTATTCTAAGTCAGA	280	64.63	-0.10	0.626	-0.199	0.312	0.442	1125.0
137	GCCCTATTCTAAGTCAGAT	281	64.73	-0.60	0.639	-0.634	0.156	0.244	1306.3
138	CCCTATTCTAAGTCAGATC	282	61.98	-0.60	0.236	-0.634	-0.094	0.024	1019.5
139	CCTATTCTAAGTCAGATCC	283	61.98	-0.60	0.236	-0.634	-0.094	-0.429	1852.3
140	CTATTCTAAGTCAGATCCT	284	60.05	-0.60	-0.046	-0.634	-0.270	-0.214	3159.3
141	TATTCTAAGTCAGATCCTA	285	57.43	-0.60	-0.430	-0.634	-0.508	-0.281	2604.8
142	ATTCTAAGTCAGATCCTAC	286	58.59	-0.60	-0.261	-0.634	-0.402	-0.345	3986.1
143	TTTCTAAGTCAGATCCTACA	287	59.91	-0.60	-0.068	-0.634	-0.283	-0.285	4500.7
144	TTCTAAGTCAGATCCTACAT	288	59.55	-0.60	-0.120	-0.634	-0.315	-0.233	4754.5
145	TCTAAGTCAGATCCTACATA	289	58.62	-0.40	-0.257	-0.460	-0.334	-0.465	3802.1
146	CTAAGTCAGATCCTACATAC	290	57.80	1.20	-0.377	0.931	0.120	-0.414	5069.4
147	TAAGTCAGATCCTACATACA	291	57.13	1.30	-0.476	1.018	0.092	-0.059	3965.2
148	AAGTCAGATCCTACATACAA	292	55.78	1.30	-0.673	1.018	-0.030	-0.034	3862.3
149	AGTCAGATCCTACATACAAA	293	55.78	1.30	-0.673	1.018	-0.030	-0.020	2868.9
150	GTCAGATCCTACATACAAAT	294	55.62	1.70	-0.697	1.366	0.087	-0.089	3542.9
151	TCAGATCCTACATACAAATC	295	54.02	1.50	-0.932	1.192	-0.125	-0.422	2477.1
152	CAGATCCTACATACAAATCA	296	54.07	1.10	-0.924	0.844	-0.252	-0.001	2522.4
153	AGATCCTACATACAAATCAT	297	52.83	1.10	-1.106	0.844	-0.365	-0.045	2554.6
154	GATCCTACATACAAATCATC	298	53.87	1.50	-0.953	1.192	-0.138	-0.031	3580.0
155	ATCCTACATACAAATCATCC	299	56.33	1.80	-0.591	1.453	0.185	-0.067	5937.7
156	TCCTACATACAAATCATCCA	300	57.54	1.80	-0.415	1.453	0.295	-0.141	4606.7
157	CCTACATACAAATCATCCAT	301	56.32	1.80	-0.594	1.453	0.184	-0.159	4877.2
158	CTACATACAAATCATCCATG	302	52.68	1.10	-1.128	0.844	-0.379	-0.278	2608.6
159	TACATACAAATCATCCATGT	303	53.56	0.30	-0.999	0.149	-0.563	-0.469	1491.7
160	ACATACAAATCATCCATGTA	304	53.56	-0.10	-0.999	-0.199	-0.695	-0.644	1364.3
161	CATACAAATCATCCATGTAT	305	53.07	-0.80	-1.071	-0.808	-0.971	-0.751	1089.8

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
162	ATACAAATCATCATGTATT	306	52.11	-1.10	-1.211	-1.069	-1.157	-0.818	1008.6
163	TACAAATCATCATGTATTG	307	52.08	-0.40	-1.215	-0.460	-0.928	-0.891	624.8
164	ACAAATCATCATGTATTGA	308	53.86	0.20	-0.955	0.062	-0.568	-0.921	535.8
165	CAATCATCATCATGTATTGAT	309	53.36	-0.50	-1.027	-0.547	-0.845	-0.860	3019.6
166	AAATCATCATCATGTATTGATA	310	51.57	-0.70	-1.291	-0.721	-1.074	-0.753	214.0
167	AATCATCATCATGTATTGATAG	311	53.47	-0.70	-1.012	-0.721	-0.901	-0.685	212.7
168	ATCATCCATGTATTGATAGAGA	312	56.66	-0.50	-0.543	-0.547	-0.545	-0.709	165.2
169	TCAATCCATGTATTGATAGAT	313	56.66	-0.10	-0.543	-0.199	-0.412	-0.686	166.0
170	CATCCATGTATTGATAGATA	314	54.80	0.30	-0.817	0.149	-0.450	-0.622	151.0
171	ATCCATGTATTGATAGATAA	315	51.69	0.30	-1.273	0.149	-0.733	-0.624	101.8
172	TCCATGTATTGATAGATAAC	316	52.19	0.30	-1.199	0.149	-0.687	-0.724	84.0
173	CCATGTATTGATAGATAACT	317	52.89	0.30	-1.097	0.149	-0.623	-0.850	130.3
174	CATGTATTGATAGATAACTA	318	48.47	0.70	-1.746	0.496	-0.894	-0.937	67.8
175	ATGTATTGATAGATAACTAT	319	47.12	0.00	-1.944	-0.112	-1.248	-1.006	65.7
176	TGTATTGATAGATAACTATG	320	47.11	-0.20	-1.945	-0.286	-1.315	-1.048	90.0
177	GTATTGATAGATAACTATGT	321	49.90	-0.20	-1.536	-0.286	-1.061	-1.099	125.9
178	TATTGATAGATAACTATGTC	322	48.24	-0.20	-1.779	-0.286	-1.212	-1.083	132.6
179	ATTGATAGATAACTATGTCT	323	50.78	-0.20	-1.407	-0.286	-0.981	-0.998	167.4
180	TTGATAGATAACTATGTCTG	324	50.75	-0.20	-1.411	-0.286	-0.984	-0.916	219.0
181	TGATAGATAACTATGTCTGG	325	53.01	-0.20	-1.080	-0.286	-0.778	-0.866	722.6
182	GATAGATAACTATGTCTGGA	326	54.36	-0.20	-0.881	-0.286	-0.655	-0.774	825.1
183	ATAGATAACTATGTCTGGAT	327	53.04	-0.10	-1.074	-0.199	-0.742	-0.679	844.4
184	TAGATAACTATGTCTGGATT	328	53.37	-0.10	-1.027	-0.199	-0.712	-0.569	912.6
185	AGATAACTATGTCTGGATTT	329	54.27	0.10	-0.895	-0.025	-0.565	-0.449	1301.8
186	GATAACTATGTCTGGATTTT	330	54.43	0.80	-0.870	0.583	-0.318	-0.335	1367.4
187	ATAACTATGTCTGGATTTTG	331	53.08	1.50	-1.070	1.192	-0.210	-0.477	1284.2
188	TAACTATGTCTGGATTTTGT	332	56.05	1.50	-0.634	1.192	0.060	-0.026	1162.5

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _M FOLD (kcal/mole @ 35 °C)	T _m Score	ΔG _M FOLD Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
189	AACATATGCTCGAATTTGTT	333	56.97	1.50	-0.499	1.192	0.144	0.084	1396.7
190	ACTATGCTCGAATTTGTTT	334	59.38	1.50	-0.145	1.192	0.363	0.176	1348.3
191	CTATGCTCGAATTTGTTTT	335	59.16	1.50	-0.177	1.192	0.343	0.264	1092.8
192	TATGCTCGAATTTGTTTT	336	57.45	1.50	-0.428	1.192	0.188	0.234	912.6
193	ATGCTCGAATTTGTTTTT	337	58.41	1.70	-0.287	1.366	0.341	0.123	994.3
194	TGCTCGAATTTGTTTTTA	338	57.81	2.00	-0.375	1.627	0.386	0.079	840.7
195	GCTCGAATTTGTTTTTAA	339	55.82	1.00	-0.667	0.757	-0.126	0.344	941.9
196	CTCGAATTTGTTTTTAAA	340	50.98	0.80	-1.377	0.583	-0.632	0.488	84.9
197	CTGGAATTTGTTTTTAAAA	341	48.16	0.30	-1.790	0.149	-1.054	0.670	78.6
198	TGGAATTTGTTTTTAAAG	342	46.41	0.10	-2.048	-0.025	-1.279	-0.851	93.2
199	GGATTTGTTTTTAAAGG	343	48.87	0.10	-1.686	-0.025	-1.055	-0.933	56.0
200	GATTTGTTTTTAAAGGC	344	50.22	0.10	-1.488	-0.025	-0.932	-0.912	49.9
201	ATTTGTTTTTAAAGGCT	345	50.84	0.10	-1.397	-0.025	-0.876	-0.843	55.0
202	TTTGTTTTTAAAGGCTC	346	52.03	0.30	-1.223	0.149	-0.702	-0.768	64.6
203	TTTGTTTTTAAAGGCTCT	347	53.64	0.50	-0.987	0.323	-0.489	0.724	162.8
204	TTGTTTTTAAAGGCTCTA	348	52.76	0.50	-1.115	0.323	-0.569	0.706	265.8
205	TGTTTTTAAAGGCTCTAA	349	50.71	0.50	-1.417	0.323	-0.756	0.677	288.5
206	GTTTTTAAAGGCTCTAAG	350	50.86	0.50	-1.395	0.323	-0.742	0.672	548.4
207	TTTTTAAAGGCTCTAAGA	351	49.40	0.70	-1.609	0.496	-0.809	0.698	524.7
208	TTTTTAAAGGCTCTAAGAT	352	49.11	1.20	-1.651	0.931	-0.670	0.746	937.9
209	TTTTTAAAGGCTCTAAGATT	353	49.11	1.20	-1.651	0.931	-0.670	0.790	1440.3
210	TTTAAAGGCTCTAAGATTT	354	49.11	1.20	-1.651	0.931	-0.670	0.820	1633.3
211	TTAAAGGCTCTAAGATTTT	355	49.11	0.50	-1.651	0.323	-0.901	0.735	1987.4
212	TAAAGGCTCTAAGATTTT	356	49.11	0.00	-1.651	-0.112	-1.067	0.627	1792.3
213	AAAAGGCTCTAAGATTTTG	357	49.63	0.20	-1.575	0.062	-0.953	0.495	2218.9
214	AAAGGCTCTAAGATTTTGT	358	54.13	1.20	-0.914	0.931	-0.213	0.365	2371.4
215	AAGGCTCTAAGATTTTGTC	359	57.38	1.20	-0.439	0.931	0.082	0.238	3308.9

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
216	AGGCTCTAAGATTTTGTCA	360	60.78	0.80	0.061	0.583	0.260	-0.087	4070.5
217	GGCTCTAAGATTTTGTCA	361	60.56	0.80	0.028	0.583	0.239	0.048	5394.5
218	GCTCTAAGATTTTGTCA	362	57.81	0.80	-0.376	0.583	-0.011	0.054	2025.5
219	CTCTAAGATTTTGTCA	363	57.81	0.80	-0.376	0.583	-0.011	-0.006	1741.9
220	TCTAAGATTTTGTCA	364	57.81	0.80	-0.376	0.583	-0.011	-0.065	1707.6
221	CTAAGATTTTGTCA	365	55.87	0.80	-0.660	0.583	-0.187	-0.089	1783.0
222	TAGATTTTGTCA	366	54.43	0.80	-0.872	0.583	-0.319	-0.076	3131.4
223	AAGATTTTGTCA	367	56.99	0.60	-0.495	0.410	-0.151	-0.082	4892.5
224	AGATTTTGTCA	368	59.39	0.60	-0.144	0.410	0.067	-0.053	5856.4
225	GATTTTGTCA	369	59.54	0.60	-0.122	0.410	0.080	0.045	6439.0
226	ATTTTGTCA	370	58.09	0.60	-0.334	0.410	-0.051	0.069	5820.3
227	TTTTGTCA	371	60.78	0.60	0.060	0.410	0.193	0.095	5189.6
228	TTTGTCA	372	61.79	0.60	0.209	0.410	0.285	0.079	4721.7
229	TTTGTCA	373	59.35	0.60	-0.149	0.410	0.063	0.075	4221.0
230	TGTCA	374	59.00	0.60	-0.200	0.410	0.032	0.056	4279.0
231	TGTCA	375	58.10	0.60	-0.333	0.410	-0.051	0.004	4102.0
232	GTCA	376	58.16	0.90	-0.324	0.670	0.054	-0.022	5069.8
233	TCATGCTACTTTGGAATAT	377	55.52	0.90	-0.711	0.670	-0.186	-0.015	2407.9
234	CATGCTACTTTGGAATAT	378	54.23	1.30	-0.900	1.018	-0.171	0.016	2443.0
235	ATGCTACTTTGGAATAT	379	56.90	1.40	-0.508	1.105	0.105	0.058	2324.3
236	TGCTACTTTGGAATAT	380	58.82	0.90	-0.227	0.670	0.114	0.099	1894.1
237	GCTACTTTGGAATAT	381	58.82	1.30	-0.227	1.018	0.246	0.180	2363.8
238	CTACTTTGGAATAT	382	57.35	1.70	-0.443	1.366	0.244	0.270	1363.0
239	TACTTTGGAATAT	383	58.39	1.70	-0.290	1.366	0.339	0.299	1217.5
240	ACTTTGGAATAT	384	58.88	1.70	-0.217	1.366	0.384	0.340	1621.8
241	CTTTGGAATAT	385	59.64	1.70	-0.106	1.366	0.453	0.346	1438.2
242	TTTGAATAT	386	57.72	1.80	-0.388	1.453	0.311	0.345	1608.0

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
243	TTGGAATATTGCTGGTGATC	387	58.73	1.80	-0.241	1.453	0.403	0.302	2334.6
244	TGGAATATTGCTGGTGATCC	388	62.18	0.50	0.266	0.323	0.288	0.244	3776.7
245	GGAATATTGCTGGTGATCCT	389	64.19	-0.20	0.561	-0.286	0.239	0.246	5648.7
246	GAATATTGCTGGTGATCCTT	390	61.99	-0.20	0.238	-0.286	0.039	0.264	5358.8
247	AATATTGCTGGTGATCCTTT	391	61.03	-0.20	0.097	-0.286	-0.049	0.316	5517.2
248	ATATTGCTGGTGATCCTTTC	392	64.63	-0.20	0.625	-0.286	0.279	0.368	6246.4
249	TATTGCTGGTGATCCTTTCC	393	68.48	-0.20	1.190	-0.286	0.629	0.444	9975.1
250	ATTGCTGGTGATCCTTTCCA	394	70.22	-0.20	1.446	-0.286	0.788	0.599	11990.0
251	TTGCTGGTGATCCTTTCCAT	395	70.22	-0.60	1.446	-0.634	0.655	0.756	11543.0
252	TGCTGGTGATCCTTTCCATC	396	71.48	-0.60	1.631	-0.634	0.770	0.862	14125.0
253	GCTGGTGATCCTTTCCATCC	397	75.32	-0.60	2.193	-0.634	1.119	0.936	23489.0
254	CTGGTGATCCTTTCCATCCC	398	74.58	-0.60	2.085	-0.634	1.052	1.022	15975.0
255	TGGTGATCCTTTCCATCCCT	399	74.58	-0.70	2.085	-0.721	1.019	1.082	16053.0
256	GGTGATCCTTTCCATCCCTG	400	74.58	-0.30	2.085	-0.373	1.151	1.136	19205.0
257	GTGATCCTTTCCATCCCTGT	401	75.40	0.20	2.206	0.062	1.391	1.080	17872.0
258	TGATCCTTTCCATCCCTGTG	402	71.89	0.20	1.691	0.062	1.072	0.955	12871.0
259	GATCCTTTCCATCCCTGTGG	403	74.58	-0.30	2.085	-0.373	1.151	0.809	8792.7
260	ATCCTTTCCATCCCTGTGGA	404	74.58	-1.60	2.085	-1.504	0.721	0.653	5609.6
261	TCCTTTCCATCCCTGTGGAA	405	72.27	-2.60	1.746	-2.373	0.181	0.454	3018.0
262	CCTTCCATCCCTGTGGAAG	406	71.00	-2.80	1.559	-2.547	-0.001	0.308	1802.6
263	CTTCCATCCCTGTGGAAGC	407	71.60	-2.80	1.648	-2.547	0.054	0.205	1074.0
264	TTTCCATCCCTGTGGAAGCA	408	70.81	-2.80	1.532	-2.547	-0.018	0.420	1132.5
265	TTCCATCCCTGTGGAAGCAC	409	71.02	-2.60	1.562	-2.373	0.067	0.074	1454.5
266	TCCATCCCTGTGGAAGCACA	410	71.74	-1.70	1.669	-1.591	0.430	0.032	1676.8
267	CCATCCCTGTGGAAGCACAT	411	70.20	-2.20	1.443	-2.025	0.125	0.026	2268.9
268	CATCCCTGTGGAAGCACATT	412	67.07	-2.20	0.983	-2.025	-0.160	0.004	1682.6
269	ATCCCTGTGGAAGCACATTG	413	65.82	-2.20	0.801	-2.025	-0.273	-0.070	1753.9

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _M FOLD (kcal/mole @ 35 °C)	T _m Score	ΔG _M FOLD Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
270	TCCTGTGGAAGCACATTGT	414	68.98	-2.20	1.263	-2.025	0.014	-0.220	1281.8
271	CCCTGTGGAAGCACATTGTA	415	66.92	-2.20	0.962	-2.025	-0.173	-0.344	1227.8
272	CCTGTGGAAGCACATTGTAC	416	63.84	-2.20	0.509	-2.025	-0.454	-0.337	700.3
273	CTGTGGAAGCACATTGTACT	417	62.01	-2.20	0.241	-2.025	-0.620	-0.307	618.7
274	TGTGGAAGCACATTGTACTG	418	59.99	-2.00	-0.056	-1.851	-0.738	-0.324	771.5
275	GTGGAAGCACATTGTACTGA	419	61.39	-0.50	0.149	-0.547	-0.115	-0.347	1180.6
276	TGGAAGCACATTGTACTGAT	420	58.35	0.50	-0.296	0.323	-0.061	-0.331	1160.5
277	GGAAGCACATTGTACTGATA	421	57.86	0.50	-0.368	0.323	-0.106	-0.239	1314.7
278	GAAGCACATTGTACTGATAT	422	55.32	0.50	-0.740	0.323	-0.336	-0.141	1102.5
279	AAGCACATTGTACTGATATC	423	55.30	0.50	-0.744	0.323	-0.339	-0.209	1222.1
280	AGCACATTGTACTGATATCT	424	59.26	0.50	-0.162	0.323	0.022	-0.302	1893.2
281	GCACATTGTACTGATATCTA	425	58.48	0.50	-0.277	0.323	-0.049	-0.398	2097.7
282	CACATTGTACTGATATCTAA	426	52.51	0.50	-1.152	0.323	-0.592	-0.446	1237.8
283	ACATTGTACTGATATCTAAT	427	51.20	0.50	-1.345	0.323	-0.711	-0.443	959.5
284	CATTGTACTGATATCTAATC	428	51.89	0.10	-1.244	-0.025	-0.781	-0.472	1149.1
285	ATTGTACTGATATCTAATCC	429	54.53	-0.30	-0.856	-0.373	-0.672	-0.490	2351.3
286	TGTACTGATATCTAATCCCT	430	58.41	-0.30	-0.287	-0.373	-0.320	-0.436	4191.6
287	TGTACTGATATCTAATCCCT	431	59.99	-0.30	-0.055	-0.373	-0.176	-0.320	5565.8
288	GTACTGATATCTAATCCCTG	432	59.99	-0.30	-0.055	-0.373	-0.176	-0.202	9980.2
289	TACTGATATCTAATCCCTGG	433	59.52	-0.30	-0.124	-0.373	-0.218	-0.084	6318.9
290	ACTGATATCTAATCCCTGGT	434	63.07	-0.30	0.397	-0.373	0.104	0.023	7749.5
291	CTGATATCTAATCCCTGGTG	435	62.43	-0.30	0.303	-0.373	0.046	0.184	8165.3
292	TGATATCTAATCCCTGGTGT	436	63.60	-0.30	0.474	-0.373	0.152	0.365	9107.6
293	GATATCTAATCCCTGGTGTC	437	65.19	0.10	0.707	-0.025	0.429	0.566	13914.0
294	ATATCTAATCCCTGGTGTC	438	65.82	1.50	0.800	1.192	0.949	0.698	15093.0
295	TATCTAATCCCTGGTGTC	439	67.41	1.50	1.033	1.192	1.093	0.822	18647.0
296	ATCTAATCCCTGGTGTC	440	69.20	1.30	1.296	1.018	1.190	0.904	21810.0

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG _{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
297	TCTAATCCCTGGTGCTCAT	441	69.20	0.80	1.296	0.583	1.025	0.996	20102.0
298	CTAATCCCTGGTGCTCATT	442	67.98	0.80	1.117	0.583	0.914	1.052	20967.0
299	TAATCCCTGGTGCTCATTG	443	65.90	0.80	0.811	0.583	0.725	1.092	18200.0
300	AATCCCTGGTGCTCATTGT	444	69.78	0.80	1.380	0.583	1.077	1.088	19845.0
301	ATCCCTGGTGCTCATTGTT	445	72.61	0.80	1.797	0.583	1.336	1.057	19231.0
302	TCCCTGGTGCTCATTGTTT	446	73.04	0.80	1.860	0.583	1.375	0.981	17629.0
303	CCCTGGTGCTCATTGTTTA	447	70.72	0.80	1.519	0.583	1.164	0.918	17009.0
304	CCTGGTGCTCATTGTTTAT	448	66.82	0.80	0.946	0.583	0.808	0.800	11580.0
305	CTGGTGCTCATTGTTTATA	449	62.17	0.80	0.264	0.583	0.386	0.600	8374.6
306	TGGTGCTCATTGTTTATAC	450	60.65	0.90	0.042	0.670	0.281	0.355	6153.3
307	GGTGCTCATTGTTTATACT	451	62.88	0.20	0.369	0.062	0.252	0.177	7134.0
308	GTGCTCATTGTTTATACTA	452	59.43	0.20	-0.138	0.062	-0.062	0.050	4435.2
309	TGTCTCATTGTTTATACTAG	453	56.35	0.20	-0.589	0.062	-0.342	-0.043	2035.5
310	GTCTCATTGTTTATACTAGG	454	59.21	0.20	-0.170	0.062	-0.082	-0.149	2466.6
311	TCTCATTGTTTATACTAGGT	455	59.21	0.20	-0.170	0.062	-0.082	-0.268	1080.9
312	CTCATTGTTTATACTAGGTA	456	57.15	0.20	-0.472	0.062	-0.269	-0.325	956.0
313	TCATTGTTTATACTAGGTAT	457	55.08	0.20	-0.776	0.062	-0.458	-0.302	529.4
314	CATTGTTTATACTAGGTATG	458	53.70	0.20	-0.978	0.062	-0.583	-0.328	471.4
315	ATTGTTTATACTAGGTATGG	459	55.01	0.20	-0.785	0.062	-0.463	-0.389	510.4
316	TGTTTATACTAGGTATGGT	460	58.17	0.20	-0.322	0.062	-0.176	-0.486	531.0
317	TGTTTATACTAGGTATGGTA	461	57.21	0.20	-0.463	0.062	-0.264	-0.560	613.3
318	GTTTATACTAGGTATGGTAA	462	55.23	0.00	-0.753	-0.112	-0.510	-0.620	685.1
319	TTTATACTAGGTATGGTAAA	463	50.42	0.00	-1.459	-0.112	-0.947	-0.639	300.0
320	TTATACTAGGTATGGTAAAT	464	50.12	0.00	-1.504	-0.112	-0.975	-0.672	316.1
321	TATACTAGGTATGGTAAATG	465	49.79	0.00	-1.551	-0.112	-1.004	-0.655	387.5
322	ATACTAGGTATGGTAAATGC	466	54.30	0.00	-0.889	-0.112	-0.594	-0.557	685.7
323	TACTAGGTATGGTAAATGCA	467	55.59	0.20	-0.700	0.062	-0.411	-0.430	759.6

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
324	ACTAGGTATGGTAAATGCAG	468	56.32	0.80	-0.593	0.583	-0.146	-0.204	1050.2
325	CTAGGTATGGTAAATGCAGT	469	58.78	1.10	-0.232	0.844	0.177	-0.157	1020.4
326	TAGGTATGGTAAATGCAGTA	470	56.24	1.10	-0.605	0.844	-0.054	-0.109	742.6
327	AGGTATGGTAAATGCAGTAT	471	56.81	1.10	-0.521	0.844	-0.002	-0.132	889.6
328	GGTATGGTAAATGCAGTATA	472	56.07	1.10	-0.631	0.844	-0.070	-0.182	858.8
329	GTATGGTAAATGCAGTATAC	473	54.02	1.10	-0.931	0.844	-0.256	-0.262	379.0
330	TATGGTAAATGCAGTATACT	474	53.06	0.40	-1.071	0.236	-0.575	-0.257	166.7
331	ATGGTAAATGCAGTATACTT	475	53.94	0.40	-0.943	0.236	-0.495	-0.249	215.3
332	TGGTAAATGCAGTATACTTC	476	55.21	0.40	-0.757	0.236	-0.380	-0.303	103.2
333	GGTAAATGCAGTATACTTCC	477	59.15	0.40	-0.178	0.236	-0.021	-0.326	246.3
334	GTAATGCAGTATACTTCCCT	478	58.53	0.80	-0.269	0.583	0.055	-0.303	163.4
335	TAAATGCAGTATACTTCCCTG	479	55.54	0.10	-0.708	-0.025	-0.448	-0.264	294.1
336	AAATGCAGTATACTTCCCTGA	480	57.36	-0.30	-0.441	-0.373	-0.415	-0.229	531.4
337	AATGCAGTATACTTCCCTGAA	481	57.36	-0.30	-0.441	-0.373	-0.415	-0.233	1995.5
338	ATGCAGTATACTTCCCTGAAG	482	59.50	-0.30	-0.128	-0.373	-0.221	-0.279	510.1
339	TGCAGTATACTTCCCTGAAGT	483	62.63	-0.90	0.332	-0.895	-0.134	-0.264	555.4
340	GCAGTATACTTCCCTGAAGTC	484	64.24	-1.10	0.568	-1.069	-0.054	-0.238	1214.0
341	CAGTATACTTCCCTGAAGTCT	485	61.94	-1.10	0.230	-1.069	-0.263	-0.237	825.7
342	AGTATACTTCCCTGAAGTCTT	486	61.00	-1.10	0.094	-1.069	-0.348	-0.264	1582.6
343	GTATACTTCCCTGAAGTCTTC	487	62.28	-1.10	0.281	-1.069	-0.232	-0.278	2391.8
344	TATACTTCCCTGAAGTCTTCA	488	60.34	-1.10	-0.004	-1.069	-0.409	-0.273	2276.3
345	ATACTTCCCTGAAGTCTTTCAT	489	60.91	-1.20	0.080	-1.156	-0.389	-0.252	2702.8
346	TACTTCCCTGAAGTCTTTCATC	490	62.40	-1.20	0.299	-1.156	-0.254	-0.274	3781.7
347	ACTTCTCTGAAGTCTTTCATCT	491	65.05	-1.20	0.686	-1.156	-0.014	-0.344	5343.4
348	CTTCTCTGAAGTCTTTCATCTA	492	63.86	-1.20	0.512	-1.156	-0.122	-0.344	6309.0
349	TTCTCTGAAGTCTTTCATCTAA	493	59.70	-1.20	-0.098	-1.156	-0.500	-0.332	6372.4
350	TCCTGAAGTCTTTCATCTAAG	494	59.55	-1.20	-0.120	-1.156	-0.513	-0.369	3835.3

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _{Mfold} (kcal/mole @ 35 °C)	T _m Score	ΔG _{Mfold} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
351	CCTGAAGTCTTTCATCTAAGG	495	60.76	-1.20	0.057	-1.156	-0.404	-0.423	8925.5
352	CTGAAGTCTTTCATCTAAGG	496	59.48	-1.20	-0.130	-1.156	-0.520	-0.472	1211.8
353	TGAAGTCTTTCATCTAAGGA	497	58.84	-1.00	-0.224	-0.982	-0.512	-0.414	609.4
354	GAAGTCTTTCATCTAAGGAA	498	56.91	-0.10	-0.507	-0.199	-0.390	-0.358	629.1
355	AAGTCTTTCATCTAAGGAACT	499	56.13	-0.10	-0.622	-0.199	-0.461	-0.344	749.3
356	AGTCTTTCATCTAAGGAACTG	500	60.12	-0.10	-0.036	-0.199	-0.098	-0.374	805.6
357	GTCTTTCATCTAAGGAACTG	501	59.84	-0.10	-0.077	-0.199	-0.124	-0.449	817.0
358	TCTTTCATCTAAGGAACTGA	502	58.11	-0.10	-0.331	-0.199	-0.281	-0.536	327.1
359	CTTTCATCTAAGGAACTGAA	503	54.95	-0.60	-0.794	-0.634	-0.733	-0.645	320.0
360	TTTCATCTAAGGAACTGAAA	504	51.39	-0.60	-1.316	-0.634	-1.057	-0.822	84.1
361	TCATCTAAGGAACTGAAAA	505	49.50	0.10	-1.595	-0.025	-0.998	-1.002	67.7
362	CATCTAAGGAACTGAAAAA	506	46.98	0.10	-1.963	-0.025	-1.227	-1.171	62.2
363	ATCTAAGGAACTGAAAAAT	507	45.78	0.10	-2.140	-0.025	-1.336	-1.298	78.9
364	TCTAAGGAACTGAAAAATA	508	45.27	0.10	-2.214	-0.025	-1.382	-1.328	43.2
365	CTAAGGAACTGAAAAATAT	509	44.36	0.10	-2.349	-0.025	-1.466	-1.322	50.4
366	TAAGGAACTGAAAAATATG	510	42.71	0.10	-2.591	-0.025	-1.616	-1.242	43.7
367	AAGGAACTGAAAAATATGC	511	46.54	0.10	-2.028	-0.025	-1.267	-1.163	45.6
368	AGGAACTGAAAAATATGCA	512	49.21	0.30	-1.637	0.149	-0.958	-1.119	49.8
369	GGAACTGAAAAATATGCAT	513	49.11	1.20	-1.651	0.931	-0.670	-1.082	53.2
370	GGAATGAAAAATATGCATC	514	47.87	1.20	-1.834	0.931	-0.783	-0.958	56.6
371	GAACTGAAAAATATGCATCA	515	46.82	0.60	-1.987	0.410	-1.076	-0.844	45.3
372	AAGTAAAAATATGCATCAC	516	46.12	0.40	-2.090	0.236	-1.206	-0.773	56.3
373	ACTGAAAAATATGCATCACC	517	51.18	0.40	-1.347	0.236	-0.746	-0.702	61.7
374	CTGAAAAATATGCATCAGCC	518	54.20	0.40	-0.905	0.236	-0.471	-0.616	224.5
375	TGAAAAATATGCATCAGCCA	519	53.65	0.60	-0.985	0.410	-0.455	-0.476	413.0
376	GAAAAATATGCATCAGCCAC	520	54.14	1.30	-0.913	1.018	-0.179	-0.289	1584.0
377	AAAAATATGCATCAGCCACA	521	54.14	1.30	-0.913	1.018	-0.179	-0.007	1846.7

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _{Mfold} (kcal/mole @ 35 °C)	T _m Score	ΔG _{Mfold} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
378	AAATATGCATCACCCACAT	522	55.78	1.10	-0.673	0.844	-0.096	0.096	2445.8
379	AAATATGCATCACCCACATC	523	58.72	0.90	-0.241	0.670	0.105	0.294	3709.4
380	AAATATGCATCACCCACATCC	524	64.13	0.90	0.552	0.670	0.597	0.494	4548.4
381	ATATGCATCACCCACATCCA	525	67.27	0.90	1.013	0.670	0.883	0.680	5254.1
382	TATGCATCACCCACATCCAG	526	67.53	0.90	1.051	0.670	0.906	0.864	5527.2
383	ATGCATCACCCACATCCAGT	527	71.21	0.90	1.590	0.670	1.241	0.991	6916.9
384	TGCATCACCCACATCCAGTA	528	70.68	0.70	1.513	0.496	1.127	1.030	5861.4
385	GCATCACCCACATCCAGTAC	529	71.39	0.70	1.617	0.496	1.191	1.043	8078.4
386	CATCACCCACATCCAGTACT	530	69.16	0.70	1.290	0.496	0.988	1.013	4148.8
387	ATCACCCACATCCAGTACTG	531	67.91	0.70	1.107	0.496	0.875	0.913	3317.1
388	TCACCCACATCCAGTACTGT	532	71.15	0.10	1.582	-0.025	0.971	0.830	2486.4
389	CACCCACATCCAGTACTGTT	533	69.94	-0.40	1.404	-0.460	0.696	0.714	2746.4
390	ACCCACATCCAGTACTGTTA	534	68.25	-0.40	1.157	-0.460	0.543	0.506	2133.0
391	CCACATCCAGTACTGTTACT	535	68.25	-0.40	1.157	-0.460	0.543	0.297	2197.0
392	CCACATCCAGTACTGTTACT	536	66.50	-0.40	0.900	-0.460	0.383	0.066	1824.0
393	CACATCCAGTACTGTTACTG	537	62.61	-1.90	0.329	-1.764	-0.467	-0.137	1675.2
394	ACATCCAGTACTGTTACTGA	538	62.71	-2.30	0.344	-2.112	-0.590	-0.313	1219.8
395	CATCCAGTACTGTTACTGAT	539	62.12	-2.30	0.258	-2.112	-0.643	-0.504	1414.0
396	ATCCAGTACTGTTACTGATT	540	61.21	-2.30	0.124	-2.112	-0.726	-0.700	1710.7
397	TCCAGTACTGTTACTGATTT	541	61.58	-2.30	0.178	-2.112	-0.692	-0.713	2280.7
398	CCAGTACTGTTACTGATTTT	542	60.48	-2.30	0.017	-2.112	-0.792	-0.659	2847.7
399	CAGTACTGTTACTGATTTTT	543	56.84	-1.90	-0.518	-1.764	-0.992	-0.635	2830.2
400	AGTACTGTTACTGATTTTTT	544	55.82	-0.30	-0.666	-0.373	-0.555	-0.588	4336.3
401	GTACTGTTACTGATTTTTTC	545	57.04	0.40	-0.488	0.236	-0.213	-0.548	6581.1
402	TACTGTTACTGATTTTTTCT	546	55.95	-0.10	-0.649	-0.199	-0.478	-0.516	5406.6
403	ACTGTTACTGATTTTTTCTT	547	56.89	-0.10	-0.510	-0.199	-0.392	-0.450	6083.1
404	CTGTTACTGATTTTTTCTTT	548	56.67	-0.10	-0.542	-0.199	-0.412	-0.482	6585.7

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
405	TGTTACTGATTTTCTTTT	549	54.96	-0.10	-0.793	-0.199	-0.567	-0.575	3923.2
406	GTTACTGATTTTCTTTT	550	55.36	-0.10	-0.734	-0.199	-0.531	-0.646	4093.5
407	TTACTGATTTTCTTTT	551	52.62	-0.10	-1.136	-0.199	-0.780	-0.730	1381.5
408	TACTGATTTTCTTTTAA	552	51.70	-0.10	-1.272	-0.199	-0.864	-0.784	1194.3
409	ACTGATTTTCTTTTAA	553	50.45	-0.10	-1.454	-0.199	-0.977	-0.746	2371.3
410	CTGATTTTCTTTTAAAC	554	50.45	-0.10	-1.454	-0.199	-0.977	-0.682	395.9
411	TGATTTTCTTTTAAACC	555	52.50	-0.10	-1.155	-0.199	-0.792	-0.583	230.7
412	GATTTTCTTTTAAACC	556	56.43	0.30	-0.578	0.149	-0.302	-0.423	314.9
413	ATTTTCTTTTAAACCCT	557	57.05	0.80	-0.487	0.583	-0.080	-0.246	276.1
414	TTTTTCTTTTAAACCCTG	558	56.99	0.80	-0.495	0.583	-0.085	-0.046	273.3
415	TTTTTCTTTTAAACCCTGC	559	60.68	0.80	0.045	0.583	0.250	0.093	628.4
416	TTTTTCTTTTAAACCCTGCG	560	60.85	0.80	0.071	0.583	0.265	0.155	4661.4
417	TTCTTTTAAACCCTGCGG	561	62.93	0.70	0.377	0.496	0.422	0.167	411.2
418	TTCTTTTAAACCCTGCGGG	562	65.01	-0.60	0.681	-0.634	0.181	0.156	289.5
419	TCCTTTTAAACCCTGCGGA	563	65.91	-1.00	0.813	-0.982	0.131	0.130	244.8
420	CTTTTAAACCCTGCGGGAT	564	64.52	-1.00	0.610	-0.982	0.005	0.096	250.7
421	TTTTTAAACCCTGCGGGATG	565	62.66	-1.00	0.337	-0.982	-0.164	0.067	207.8
422	TTTTTAAACCCTGCGGGATGT	566	65.23	-1.00	0.713	-0.982	0.069	0.406	255.8
423	TTTAAACCCTGCGGGATGTG	567	64.80	-1.00	0.651	-0.982	0.030	0.442	356.8
424	TTTAAACCCTGCGGGATGTGG	568	66.83	-1.00	0.949	-0.982	0.215	0.204	497.8
425	TTAACCCTGCGGGATGTGGT	569	69.50	-1.00	1.339	-0.982	0.457	0.348	754.3
426	TAACCCTGCGGGATGTGTA	570	68.63	-1.00	1.212	-0.982	0.378	0.434	902.4
427	AACCCTGCGGGATGTGGTAT	571	69.14	-1.00	1.286	-0.982	0.424	0.555	1186.6
428	ACCCTGCGGGATGTGGTATT	572	71.66	-1.00	1.657	-0.982	0.654	0.595	1514.9
429	CCCTGCGGGATGTGGTATTC	573	72.66	-0.60	1.804	-0.634	0.878	0.569	2407.6
430	CCTGCGGGATGTGGTATCC	574	72.66	-0.60	1.804	-0.634	0.878	0.526	3019.4
431	CTGCGGGATGTGGTATTCCT	575	71.02	-1.30	1.563	-1.243	0.497	0.426	3275.3

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
432	TGCGGATGTGGTATTCCTA	576	68.54	-1.30	1.199	-1.243	0.271	0.294	2830.8
433	GCGGGATGTGGTATTCCTAA	577	66.48	-1.30	0.896	-1.243	0.083	0.408	2620.5
434	CGGGATGTGGTATTCCTAAT	578	62.46	-1.30	0.307	-1.243	-0.282	-0.058	1827.8
435	GGGATGTGGTATTCCTAATT	579	62.37	-1.30	0.294	-1.243	-0.290	-0.244	1957.4
436	GGATGTGGTATTCCTAATTG	580	59.71	-0.90	-0.097	-0.895	-0.400	-0.330	1686.2
437	GATGTGGTATTCCTAATTGA	581	58.45	-0.20	-0.281	-0.286	-0.283	-0.396	1395.0
438	ATGTGGTATTCCTAATTGAA	582	55.24	-0.20	-0.752	-0.286	-0.575	-0.444	1245.7
439	TGTGGTATTCCTAATTGAAC	583	55.76	-0.30	-0.675	-0.373	-0.561	-0.473	1314.0
440	GTGGTATTCCTAATTGAACT	584	57.73	-0.30	-0.387	-0.373	-0.382	-0.470	1818.7
441	TGGTATTCCTAATTGAACTT	585	55.15	-0.30	-0.765	-0.373	-0.616	-0.474	880.3
442	GGTATTCCTAATTGAACTTC	586	56.47	-0.30	-0.572	-0.373	-0.496	-0.443	1419.0
443	GTATTCCTAATTGAACTTCC	587	57.76	-0.30	-0.383	-0.373	-0.379	-0.343	1567.9
444	TATTCCTAATTGAACTTCCC	588	58.57	-0.30	-0.264	-0.373	-0.306	-0.248	1959.4
445	ATTCCTAATTGAACTTCCCA	589	60.26	-0.30	-0.016	-0.373	-0.152	-0.164	2971.8
446	TTCCTAATTGAACTTCCCAG	590	60.45	-0.10	0.013	-0.199	-0.068	-0.200	1898.5
447	TCCTAATTGAACTTCCCAGA	591	61.36	0.70	0.146	0.496	0.279	-0.300	1392.3
448	CCTAATTGAACTTCCCAGAA	592	58.27	0.70	-0.308	0.496	-0.002	-0.397	1143.2
449	CTAATTGAACTTCCCAGAAG	593	54.92	-0.70	-0.800	-0.721	-0.770	-0.467	427.7
450	TAATTGAACTTCCCAGAAGT	594	55.84	-1.90	-0.664	-1.764	-1.082	-0.545	148.5
451	AATTGAACTTCCCAGAAGTC	595	57.61	-2.10	-0.404	-1.938	-0.987	-0.677	259.1
452	ATTGAACTTCCCAGAAGTCT	596	61.42	-2.10	0.154	-1.938	-0.641	-0.751	241.9
453	TTGAACTTCCCAGAAGTCTT	597	61.76	-2.10	0.205	-1.938	-0.609	-0.730	808.1
454	TGAACCTTCCCAGAAGTCTTG	598	61.34	-2.10	0.143	-1.938	-0.648	-0.586	351.6
455	GAACTTCCCAGAAGTCTTGA	599	62.71	-2.10	0.344	-1.938	-0.523	-0.445	499.7
456	AACTTCCCAGAAGTCTTGAG	600	61.63	-2.10	0.186	-1.938	-0.621	-0.262	407.4
457	ACTTCCCAGAAGTCTTGAGT	601	66.97	-1.90	0.969	-1.764	-0.069	-0.138	492.1
458	CTTCCCAGAAGTCTTGAGTT	602	66.75	-1.00	0.937	-0.982	0.208	-0.049	736.1

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _M ^{FOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG _M ^{FOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
459	TTCCAGAAAGTCTTGAGTTC	603	66.31	-0.20	0.872	-0.286	0.432	0.058	815.2
460	TCCAGAGTCTTGAGTTC	604	67.98	-1.20	1.116	-1.156	0.253	0.404	888.8
461	CCAGAAAGTCTTGAGTTC	605	67.98	-1.40	1.116	-1.330	0.187	0.049	2021.6
462	CCAGAAAGTCTTGAGTTC	606	66.10	-1.40	0.842	-1.330	0.017	-0.013	1988.5
463	CAGAAAGTCTTGAGTTC	607	62.41	-1.40	0.300	-1.330	-0.319	-0.082	2008.8
464	AGAAAGTCTTGAGTTC	608	60.43	-1.20	0.009	-1.156	-0.434	-0.405	2631.8
465	GAAGTCTTGAGTTC	609	60.20	-0.50	-0.025	-0.547	-0.223	-0.151	3052.8
466	AAGTCTTGAGTTC	610	59.12	0.30	-0.183	0.149	-0.057	-0.242	3509.3
467	AGTCTTGAGTTC	611	60.75	0.30	0.056	0.149	0.091	-0.244	3221.6
468	GTCTTGAGTTC	612	58.29	0.30	-0.305	0.149	-0.132	-0.246	3677.1
469	TCTTGAGTTC	613	55.25	0.30	-0.751	0.149	-0.409	-0.238	1176.6
470	CTTGAGTTC	614	57.04	0.10	-0.488	-0.025	-0.312	-0.256	1168.1
471	TGAGTTC	615	55.29	0.10	-0.745	-0.025	-0.471	-0.292	666.3
472	TGAGTTC	616	56.35	0.10	-0.589	-0.025	-0.375	-0.274	674.0
473	GAGTTC	617	58.57	0.10	-0.263	-0.025	-0.173	-0.256	1471.4
474	AGTTC	618	58.61	0.10	-0.257	-0.025	-0.169	-0.240	1493.5
475	GTTCTCT	619	60.59	0.10	0.032	-0.025	0.011	-0.247	2191.5
476	TTCTCTT	620	57.16	0.10	-0.471	-0.025	-0.301	-0.347	1410.3
477	TCTCTT	621	58.23	0.10	-0.314	-0.025	-0.204	-0.443	1262.8
478	CTCTT	622	54.79	0.10	-0.817	-0.025	-0.516	-0.549	1072.9
479	TCTT	623	50.95	0.10	-1.382	-0.025	-0.866	-0.629	540.9
480	CTT	624	49.77	0.50	-1.554	0.323	-0.841	-0.695	539.2
481	TTATT	625	48.99	0.50	-1.668	0.323	-0.912	-0.768	709.0
482	TATT	626	50.64	0.50	-1.427	0.323	-0.762	-0.775	978.1
483	ATTA	627	50.64	0.50	-1.427	0.323	-0.762	-0.732	1217.7
484	TTA	628	51.15	0.50	-1.352	0.323	-0.716	-0.693	1748.1
485	TA	629	52.79	0.50	-1.112	0.323	-0.567	-0.646	2511.5

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
486	AAGTTCTCTGAAATCTACTA	630	52.79	0.50	-1.112	0.323	-0.567	-0.643	2997.2
487	AGTTCTCTGAAATCTACTAA	631	52.79	0.50	-1.112	0.323	-0.567	-0.663	2887.6
488	GTTCTCTGAAATCTACTAAT	632	52.65	0.50	-1.133	0.323	-0.580	-0.725	4421.3
489	TTCTCTGAAATCTACTAATT	633	50.14	0.70	-1.500	0.496	-0.741	-0.832	1937.7
490	TCCTGAAATCTACTAATTT	634	50.14	0.20	-1.500	0.062	-0.906	-0.962	1773.3
491	CTCTGAAATCTACTAATTTT	635	49.31	-0.30	-1.622	-0.373	-1.147	-1.102	1491.1
492	TCGAAATCTACTAATTTTC	636	48.55	-0.60	-1.734	-0.634	-1.316	-1.171	376.6
493	CTGAAATCTACTAATTTCT	637	49.31	-1.30	-1.622	-1.243	-1.478	-1.178	371.9
494	TGAAATCTACTAATTTTCTC	638	48.55	-1.30	-1.734	-1.243	-1.547	-1.092	415.2
495	GAAATCTACTAATTTTCTCC	639	52.45	-0.90	-1.161	-0.895	-1.060	-0.938	1097.9
496	AAATCTACTAATTTTCTCCA	640	52.47	-0.10	-1.158	-0.199	-0.794	-0.778	1429.1
497	AATCTACTAATTTTCTCCAT	641	54.25	0.90	-0.897	0.670	-0.301	-0.620	1812.5
498	ATCTACTAATTTTCTCCATT	642	56.46	1.00	-0.572	0.757	-0.067	-0.485	1943.4
499	TCTACTAATTTTCTCCATTT	643	56.80	0.50	-0.523	0.323	-0.202	-0.421	1506.1
500	CTACTAATTTTCTCCATTTA	644	54.93	0.50	-0.797	0.323	-0.372	-0.376	1694.7
501	TACTAATTTTCTCCATTAG	645	53.14	0.30	-1.060	0.149	-0.600	-0.396	946.7
502	ACTAATTTTCTCCATTTAGT	646	56.69	-0.70	-0.539	-0.721	-0.608	-0.407	1114.3
503	CTAATTTTCTCCATTTAGTA	647	55.57	0.00	-0.704	-0.112	-0.479	-0.369	963.9
504	TAATTTTCTCCATTTAGTAC	648	54.12	0.50	-0.917	0.323	-0.446	-0.274	1347.9
505	AAATTTTCTCCATTTAGTACT	649	56.69	0.70	-0.539	0.496	-0.145	-0.430	2067.7
506	ATTTTCTCCATTTAGTACTG	650	58.66	0.80	-0.250	0.583	0.067	0.037	2724.2
507	TTTTTCTCCATTTAGTACTGT	651	61.92	0.60	0.228	0.410	0.297	0.486	3367.9
508	TTTCTCCATTTAGTACTGTC	652	63.10	0.60	0.401	0.410	0.404	0.344	5235.8
509	TTCTCCATTTAGTACTGTCT	653	64.84	0.60	0.656	0.410	0.562	0.377	6423.5
510	TCCTCATTAGTACTGTCTT	654	64.84	0.60	0.656	0.410	0.562	0.396	7758.9
511	CTCCATTTAGTACTGTCTTT	655	63.63	0.60	0.479	0.410	0.453	0.342	8001.5
512	TCCATTTAGTACTGTCTTTT	656	61.92	0.60	0.228	0.410	0.297	0.273	5512.4

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
513	CCATTAGTACTGCTTTT	657	60.78	0.60	0.061	0.410	0.194	0.240	5300.0
514	CATTAGTACTGCTTTT	658	57.04	0.80	-0.489	0.583	-0.081	0.147	3902.1
515	ATTAGTACTGCTTTTTC	659	57.08	0.80	-0.482	0.583	-0.077	0.099	4641.8
516	TTTAGTACTGCTTTTCT	660	59.26	0.80	-0.162	0.583	0.121	0.084	4888.4
517	TTAGTACTGCTTTTCTT	661	59.26	0.80	-0.162	0.583	0.121	0.160	5477.3
518	TAGTACTGCTTTTCTTT	662	59.26	0.80	-0.162	0.583	0.121	0.242	5064.9
519	AGTACTGCTTTTCTTTA	663	59.26	1.00	-0.162	0.757	0.187	0.340	5580.3
520	GTAAGTCTTTTCTTTAT	664	59.04	2.70	-0.195	2.236	0.729	0.400	5478.3
521	TACTGCTTTTCTTTATG	665	55.71	2.90	-0.683	2.410	0.492	0.480	2275.5
522	ACTGCTTTTCTTTATGG	666	59.07	1.70	-0.190	1.366	0.402	0.524	1730.8
523	CTGCTTTTCTTTATGGC	667	62.92	1.70	0.374	1.366	0.751	0.440	2405.5
524	TGCTTTTCTTTATGGCA	668	62.14	1.70	0.260	1.366	0.680	0.258	1942.0
525	GTCTTTTCTTTATGCAA	669	60.05	1.50	-0.047	1.192	0.424	0.068	2085.6
526	TCCTTTTCTTTATGCAAA	670	54.99	0.60	-0.788	0.410	-0.333	-0.406	493.2
527	CTTTTCTTTATGGCAAT	671	53.75	0.10	-0.971	-0.025	-0.612	-0.309	532.7
528	TTTTTCTTTATGGCAATA	672	51.30	0.10	-1.331	-0.025	-0.835	-0.507	280.0
529	TTTTTCTTTATGGCAATAC	673	51.49	0.10	-1.302	-0.025	-0.817	-0.640	440.8
530	TTTTTCTTTATGGCAATACT	674	53.08	0.10	-1.069	-0.025	-0.672	-0.652	463.1
531	TTTCTTTATGGCAAAFACTG	675	52.74	0.10	-1.119	-0.025	-0.704	-0.630	579.0
532	TTCTTTATGGCAAAFACTGG	676	54.90	0.10	-0.802	-0.025	-0.507	-0.572	673.7
533	TCCTTTATGGCAAAFACTGGA	677	55.85	0.10	-0.663	-0.025	-0.421	-0.504	837.0
534	CTTTATGGCAAAFACTGGAG	678	54.78	0.10	-0.820	-0.025	-0.518	-0.490	1061.9
535	TTATGGCAAAFACTGGAGT	679	55.74	0.30	-0.679	0.149	-0.365	-0.507	855.0
536	TTATGGCAAAFACTGGAGTA	680	54.87	0.60	-0.806	0.410	-0.344	-0.562	775.0
537	TATGGCAAAFACTGGAGTAT	681	54.56	0.00	-0.852	-0.112	-0.571	-0.591	773.6
538	ATGGCAAAFACTGGAGTATT	682	55.42	-1.00	-0.726	-0.982	-0.823	-0.647	702.5
539	TGGCAAAFACTGGAGTATTG	683	55.37	-1.20	-0.733	-1.156	-0.893	-0.775	387.5

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
540	GGCAATACTGGAGTATGT	684	58.33	-1.20	-0.298	-1.156	-0.624	-0.924	435.3
541	GCAATACTGGAGTATGTA	685	55.24	-1.20	-0.753	-1.156	-0.906	-0.974	93.7
542	CAAATACTGGAGTATGTAT	686	51.30	-1.20	-1.331	-1.156	-1.264	-0.913	50.0
543	AAATACTGGAGTATGTATG	687	49.96	-1.20	-1.527	-1.156	-1.386	-0.809	50.4
544	AATACTGGAGTATGTATGG	688	54.30	-1.00	-0.890	-0.982	-0.925	-0.688	64.7
545	ATACTGGAGTATGTATGGA	689	57.60	-0.30	-0.406	-0.373	-0.394	-0.483	76.0
546	TACTGGAGTATGTATGGAT	690	57.60	0.40	-0.406	0.236	-0.162	-0.236	86.0
547	ACTGGAGTATGTATGGATT	691	58.53	1.30	-0.269	1.018	0.220	-0.009	123.4
548	CTGGAGTATGTATGGATTC	692	59.39	2.00	-0.144	1.627	0.529	0.135	121.5
549	TGGAGTATGTATGGATTCT	693	59.39	1.80	-0.144	1.453	0.463	0.210	641.3
550	GGAGTATGTATGGATTCTC	694	60.95	0.60	0.086	0.410	0.209	0.286	161.5
551	GAGTATGTATGGATTCTCA	695	59.52	0.60	-0.124	0.410	0.079	0.321	129.9
552	AGTATGTATGGATTCTCAG	696	58.31	1.10	-0.302	0.844	0.134	0.371	88.7
553	GATATGTATGGATTCTCAGG	697	60.87	1.10	0.074	0.844	0.367	0.462	112.5
554	TATGTATGGATTCTCAGGC	698	61.97	1.10	0.236	0.844	0.467	0.575	134.6
555	ATTGTATGGATTCTCAGGCC	699	66.52	1.10	0.902	0.844	0.880	0.669	191.6
556	TTGTATGGATTCTCAGGCC	700	70.34	0.70	1.463	0.496	1.096	0.714	254.5
557	TGTATGGATTCTCAGGCCCA	701	71.11	0.20	1.577	0.062	1.001	0.738	332.2
558	GTATGGATTCTCAGGCCCAA	702	68.95	0.00	1.259	-0.112	0.738	0.761	415.6
559	TATGGATTCTCAGGCCCAAT	703	65.78	0.00	0.795	-0.112	0.450	0.774	285.0
560	ATGGATTCTCAGGCCCAATT	704	66.68	0.00	0.925	-0.112	0.531	0.737	464.0
561	TGGATTCTCAGGCCCAATTT	705	67.04	0.20	0.979	0.062	0.630	0.663	492.5
562	GGATTCTCAGGCCCAATTTT	706	67.51	1.10	1.048	0.844	0.970	0.624	639.7
563	GATTCTCAGGCCCAATTTTT	707	65.34	1.30	0.729	1.018	0.839	0.595	512.4
564	ATTCTCAGGCCCAATTTTTG	708	63.94	0.60	0.524	0.410	0.481	0.513	393.4
565	TTCTCAGGCCCAATTTTTGA	709	65.24	0.20	0.716	0.062	0.467	0.394	334.3
566	TCTCAGGCCCAATTTTTGAA	710	62.85	0.20	0.364	0.062	0.249	0.181	308.2

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
567	CTCAGGCCCAATTTTGAAA	711	59.62	0.20	-0.109	0.062	-0.044	-0.048	199.2
568	TCAGGCCCAATTTTGAAAAT	712	57.85	0.20	-0.369	0.062	-0.205	-0.223	164.3
569	CAGGCCCAATTTTGAAAAT	713	56.95	-0.50	-0.501	-0.547	-0.518	-0.412	125.6
570	AGGCCCAATTTTGAAAATTT	714	56.09	-1.00	-0.627	-0.982	-0.762	-0.574	102.6
571	GGCCCAATTTTGAAAATTTT	715	56.23	-1.00	-0.606	-0.982	-0.749	-0.688	91.6
572	GCCCAATTTTGAAAATTTTC	716	55.07	-1.00	-0.777	-0.982	-0.855	-0.806	76.2
573	CCCAATTTTGAAAATTTTCC	717	54.96	-1.00	-0.792	-0.982	-0.864	-0.881	78.8
574	CAAATTTTGAAAATTTTCCC	718	54.96	-1.00	-0.792	-0.982	-0.864	-0.841	84.8
575	CAATTTTGAAAATTTTCCCT	719	53.17	-1.00	-1.055	-0.982	-1.027	-0.755	162.0
576	AATTTTGAAAATTTTCCCTT	720	52.25	-0.80	-1.190	-0.808	-1.045	-0.634	539.5
577	ATTTTGAAAATTTTCCCTTC	721	55.17	0.10	-0.762	-0.025	-0.482	-0.514	1787.3
578	TTTTTGAAAATTTTCCCTTCC	722	58.88	0.10	-0.219	-0.025	-0.145	-0.389	6354.2
579	TTTGAATTTTCCCTTCCCT	723	60.39	0.10	0.004	-0.025	-0.007	-0.243	9513.6
580	TTGAATTTTCCCTTCCCTT	724	60.39	0.10	0.004	-0.025	-0.007	-0.062	10660.0
581	TGAATTTTCCCTTCCCTTT	725	60.39	0.10	0.004	-0.025	-0.007	0.407	11202.0
582	TGAATTTTCCCTTCCCTTTT	726	60.39	0.10	0.004	-0.025	-0.007	0.293	11543.0
583	GAAATTTTCCCTTCCCTTTC	727	61.81	0.40	0.212	0.236	0.221	0.596	14774.0
584	AAATTTTCCCTTCCCTTTTCC	728	64.17	1.20	0.557	0.931	0.699	0.952	18197.0
585	AATTTTCCCTTCCCTTTTCCA	729	67.39	1.70	1.030	1.366	1.158	1.307	21410.0
586	ATTTTCCCTTCCCTTTTCCAT	730	69.58	4.00	1.351	3.366	2.117	1.679	22869.0
587	TTTCCCTTCCCTTTTCCATT	731	69.96	5.00	1.408	4.236	2.482	2.039	21818.0
588	TTCCCTTCCCTTTTCCATT	732	69.96	5.00	1.408	4.236	2.482	2.113	21341.0
589	TCCCTTCCCTTTTCCATTTC	733	71.19	5.00	1.588	4.236	2.594	2.085	22063.0
590	TCCCTTCCCTTTTCCATTCT	734	72.77	5.00	1.820	4.236	2.738	1.863	22152.0
591	CCCTTCCCTTTTCCATTCTG	735	71.01	0.90	1.561	0.670	1.223	1.571	20764.0
592	CCTTCCCTTTTCCATTCTGT	736	70.68	0.20	1.513	0.062	0.961	1.289	12579.0
593	CTTCCCTTTTCCATTCTGTA	737	66.30	0.20	0.870	0.062	0.563	0.945	9036.3

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
594	TTCTTTTCCATTCTGTAC	738	64.87	0.20	0.660	0.062	0.433	0.505	8251.8
595	TCCTTTTCCATTCTGTACA	739	65.74	0.20	0.788	0.062	0.512	0.257	20788.0
596	CCCTTTTCCATTCTGTACAA	740	62.11	0.20	0.256	0.062	0.182	0.024	7073.9
597	CTTTTCCATTCTGTACAAA	741	56.39	0.20	-0.583	0.062	-0.338	-0.153	2932.4
598	TTTTCATTCTGTACAAAT	742	54.49	0.20	-0.862	0.062	-0.511	-0.300	1897.3
599	TTTTCATTCTGTACAAAT	743	54.49	-0.30	-0.862	-0.373	-0.676	-0.449	2158.1
600	TTCCATTCTGTACAAATTT	744	54.49	-0.30	-0.862	-0.373	-0.676	-0.608	2215.9
601	TCATTCTGTACAAATTTT	745	55.43	-0.30	-0.724	-0.373	-0.591	-0.605	2168.6
602	CCATTCTGTACAAATTTCT	746	56.07	-0.30	-0.631	-0.373	-0.533	-0.708	2025.8
603	CATTCTGTACAAATTTCTA	747	51.65	-0.30	-1.278	-0.373	-0.934	-0.708	1277.2
604	ATTCTGTACAAATTTCTAC	748	50.83	-0.10	-1.398	-0.199	-0.943	-0.736	1944.8
605	TTCTGTACAAATTTCTACT	749	52.78	0.40	-1.112	0.236	-0.600	-0.790	2504.3
606	TTCTGTACAAATTTCTACTA	750	51.90	0.40	-1.242	0.236	-0.681	-0.876	2941.5
607	TCGTACAAATTTCTACTAA	751	49.84	0.40	-1.544	0.236	-0.868	-0.846	2694.8
608	CTGTACAAATTTCTACTAAT	752	48.73	0.40	-1.707	0.236	-0.969	-0.827	2610.7
609	TGTACAAATTTCTACTAATG	753	46.88	0.40	-1.979	0.236	-1.137	-0.845	1678.1
610	GTACAAATTTCTACTAATGC	754	50.66	0.60	-1.424	0.410	-0.727	-0.854	5877.3
611	TACAAATTTCTACTAATGCT	755	49.82	0.60	-1.547	0.410	-0.803	-0.849	4461.0
612	ACAAATTTCTACTAATGCTT	756	50.65	0.60	-1.425	0.410	-0.728	-0.816	5943.2
613	CAAAATTTCTACTAATGCTTT	757	50.46	0.60	-1.453	0.410	-0.745	-0.753	6492.9
614	AAATTTCTACTAATGCTTTT	758	49.47	0.60	-1.599	0.410	-0.836	-0.745	6875.0
615	AATTTCTACTAATGCTTTTA	759	50.61	0.60	-1.431	0.410	-0.731	-0.727	7950.3
616	ATTCTACTAATGCTTTTAT	760	52.40	0.20	-1.169	0.062	-0.701	-0.749	8314.8
617	TTTCTACTAATGCTTTTATT	761	52.72	0.20	-1.122	0.062	-0.672	-0.720	6885.8
618	TTCTACTAATGCTTTTATTT	762	52.72	0.20	-1.122	0.062	-0.672	-0.730	6443.2
619	TCTACTAATGCTTTTATTTT	763	52.72	0.20	-1.122	0.062	-0.672	-0.731	6331.0
620	CTACTAATGCTTTTATTTT	764	51.81	0.20	-1.255	0.062	-0.755	-0.748	5952.5

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
621	TACTAATGCTTTTATTTTT	765	50.18	0.20	-1.494	0.062	-0.903	-0.724	2662.8
622	ACTAATGCTTTTATTTTTTC	766	51.96	0.20	-1.233	0.062	-0.741	-0.667	3034.0
623	CTAATGCTTTTATTTTTTCT	767	53.41	0.20	-1.021	0.062	-0.609	-0.513	2198.5
624	TAATGCTTTTATTTTTTCTT	768	51.76	0.40	-1.263	0.236	-0.694	-0.315	1670.1
625	AATGCTTTTATTTTTTCTTC	769	53.61	1.10	-0.992	0.844	-0.294	-0.038	3039.4
626	ATGCTTTTATTTTTTCTTCT	770	57.66	2.10	-0.397	1.714	0.405	0.177	3873.8
627	TGCTTTTATTTTTTCTTCTG	771	57.60	2.80	-0.406	2.323	0.631	0.363	3609.7
628	GCTTTTATTTTTTCTTCTGT	772	60.96	3.10	0.087	2.583	1.036	0.464	4891.4
629	CTTTTATTTTTTCTTCTGTC	773	57.96	3.10	-0.353	2.583	0.763	0.480	3071.6
630	TTTATTTTTTCTTCTGTGCA	774	57.22	3.10	-0.461	2.583	0.696	0.394	2667.2
631	TTTATTTTTTCTTCTGTCAA	775	54.81	1.70	-0.816	1.366	0.013	0.312	2293.1
632	TATTTTTTCTTCTGTCAAT	776	54.46	1.20	-0.866	0.931	-0.183	0.232	2123.0
633	TATTTTTTCTTCTGTCAATG	777	54.08	1.20	-0.922	0.931	-0.218	0.237	1914.7
634	ATTTTTTCTTCTGTCAATGG	778	57.36	1.20	-0.442	0.931	0.080	0.263	2174.1
635	TTTTTCTTCTGTCAATGGC	779	61.67	1.20	0.192	0.931	0.473	0.372	3659.7
636	TTTTTCTTCTGTCAATGGCC	780	65.26	1.20	0.717	0.931	0.799	0.509	5217.7
637	TTTTTCTTCTGTCAATGGCCA	781	66.11	1.20	0.843	0.931	0.877	0.569	4559.7
638	TTTCTTCTGTCAATGGCCAT	782	65.73	1.00	0.787	0.757	0.776	0.576	4347.7
639	TTCTTCTGTCAATGGCCATT	783	65.73	1.00	0.787	0.757	0.776	0.506	5267.4
640	TCTTCTGTCAATGGCCATTG	784	65.26	-0.60	0.718	-0.634	0.204	0.389	3922.8
641	CTTCTGTCAATGGCCATTGT	785	66.97	-1.30	0.968	-1.243	0.128	0.235	3608.6
642	TTCTGTCAATGGCCATTGTT	786	65.36	-1.30	0.733	-1.243	-0.018	0.044	1881.6
643	TCTGTCAATGGCCATTGTTT	787	65.36	-1.30	0.733	-1.243	-0.018	-0.139	1658.0
644	CTGTCAATGGCCATTGTTTA	788	63.32	-1.30	0.433	-1.243	-0.204	-0.255	1369.8
645	TGTCAATGGCCATTGTTTAA	789	59.38	-1.30	-0.144	-1.243	-0.562	-0.353	605.8
646	GTCATGGCCATTGTTTAAAC	790	59.99	-1.30	-0.055	-1.243	-0.506	-0.357	933.2
647	TCAATGGCCATTGTTTAACT	791	58.93	-1.30	-0.211	-1.243	-0.603	-0.334	441.8

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
648	CAATGGCCATTGTTAACTT	792	57.97	-0.90	-0.352	-0.895	-0.558	-0.284	545.6
649	AATGGCCATTGTTAACTTT	793	57.07	0.90	-0.483	0.670	-0.045	-0.173	781.4
650	ATGGCCATTGTTAACTTTT	794	59.31	0.90	-0.156	0.670	0.158	-0.092	1027.3
651	TGGCCATTGTTAACTTTTG	795	59.24	0.90	-0.165	0.670	0.152	0.024	1102.5
652	GGCCATTGTTAACTTTTGG	796	61.84	0.30	0.216	0.149	0.190	0.156	935.7
653	GCCATTGTTAACTTTTGGG	797	61.84	-0.10	0.216	-0.199	0.058	0.248	403.7
654	CCATTGTTAACTTTTGGGC	798	61.84	0.30	0.216	0.149	0.190	0.254	269.3
655	CATTGTTAACTTTTGGGCC	799	61.84	0.90	0.216	0.670	0.389	0.299	296.8
656	ATTGTTAACTTTTGGGCCA	800	61.84	0.90	0.216	0.670	0.389	0.367	449.4
657	TGTTTAACTTTTGGGCCAT	801	61.84	0.90	0.216	0.670	0.389	0.377	448.1
658	TGTTTAACTTTTGGGCCATC	802	62.91	0.90	0.373	0.670	0.486	0.340	584.9
659	GTTTAACTTTTGGGCCATCC	803	66.73	0.40	0.934	0.236	0.669	0.275	1032.4
660	TTTAACTTTTGGGCCATCCA	804	64.79	-0.70	0.649	-0.721	0.128	0.235	737.8
661	TTAACTTTTGGGCCATCCAT	805	64.44	-1.20	0.598	-1.156	-0.069	0.274	950.2
662	TAACTTTTGGGCCATCCATT	806	64.44	-1.20	0.598	-1.156	-0.069	0.340	1308.0
663	AATTTTGGGCCATCCATTC	807	66.42	-1.20	0.888	-1.156	0.111	0.296	2360.1
664	ACTTTTGGGCCATCCATTCC	808	72.21	-1.20	1.738	-1.156	0.638	0.387	4946.0
665	CTTTTGGGCCATCCATTCT	809	73.53	-1.20	1.930	-1.156	0.758	0.489	6789.2
666	TTTGGGCCATCCATTCCTG	810	71.49	-1.20	1.632	-1.156	0.573	0.560	8150.6
667	TTTGGGCCATCCATTCCTGG	811	73.62	-1.20	1.945	-1.156	0.766	0.622	7589.0
668	TGGGCCATCCATTCCTGGCT	812	77.43	-2.80	2.504	-2.547	0.584	0.580	13914.0
669	TGGGCCATCCATTCCTGGCT	813	78.94	-3.50	2.725	-3.156	0.490	0.500	17513.0
670	GGGCATCCATTCCTGGCTT	814	79.51	-3.50	2.809	-3.156	0.542	0.449	19883.0
671	GGGCATCCATTCCTGGCTTT	815	77.37	-3.50	2.494	-3.156	0.347	0.324	20103.0
672	GCCATCCATTCCTGGCTTTA	816	74.28	-3.10	2.040	-2.808	0.198	0.244	18622.0
673	CCATCCATTCCTGGCTTTAA	817	67.92	-1.30	1.109	-1.243	0.215	0.422	16915.0
674	CATCCATTCCTGGCTTTAAT	818	64.36	-1.30	0.585	-1.243	-0.109	0.028	13910.0

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG _{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
675	ATCCATTCTGGCTTTAAT	819	63.53	-1.30	0.464	-1.243	-0.185	-0.009	12524.0
676	TCCATTCCTGGCTTTAAT	820	63.88	-1.30	0.516	-1.243	-0.152	-0.005	11890.0
677	CCATTCCTGGCTTTAAT	821	62.81	-0.90	0.359	-0.895	-0.118	0.040	12839.0
678	CATTCCTGGCTTTAAT	822	58.55	0.90	-0.266	0.670	0.090	0.126	9726.8
679	ATTCCTGGCTTTAAT	823	57.84	1.50	-0.371	1.192	0.223	0.238	8499.7
680	TTCTGGCTTTAAT	824	59.78	1.90	-0.086	1.540	0.532	0.336	6800.4
681	TCCTGGCTTTAAT	825	59.37	1.90	-0.146	1.540	0.494	0.306	5445.6
682	CCTGGCTTTAAT	826	60.53	1.90	0.024	1.540	0.600	0.434	2901.6
683	CTGGCTTTAAT	827	59.77	1.90	-0.087	1.540	0.531	0.434	1174.2
684	TGGCTTTAAT	828	57.25	1.90	-0.458	1.540	0.301	0.268	521.3
685	GGCTTTAAT	829	57.86	1.90	-0.368	1.540	0.357	0.066	611.1
686	GCTTTAAT	830	56.55	1.80	-0.560	1.453	0.205	-0.148	287.6
687	CTTTAAT	831	52.66	0.40	-1.130	0.236	-0.611	-0.330	109.5
688	TTTAAT	832	53.62	-0.80	-0.989	-0.808	-0.920	-0.454	59.5
689	TTAAT	833	54.59	-1.00	-0.847	-0.982	-0.898	-0.540	62.1
690	TAAAT	834	56.28	-1.00	-0.599	-0.982	-0.745	-0.632	59.4
691	AAAT	835	58.27	-1.00	-0.308	-0.982	-0.564	-0.613	68.0
692	ATTTACTGGTACAGTCTCA	836	61.78	-1.00	0.207	-0.982	-0.245	-0.564	72.9
693	TTTTACTGGTACAGTCTCA	837	59.61	-1.00	-0.111	-0.982	-0.442	-0.515	62.2
694	TTTACTGGTACAGTCTCAAT	838	59.25	-1.00	-0.164	-0.982	-0.475	-0.439	64.5
695	TTACTGGTACAGTCTCAATA	839	58.30	-1.00	-0.303	-0.982	-0.561	-0.348	53.5
696	TACTGGTACAGTCTCAATAG	840	58.15	-1.00	-0.326	-0.982	-0.575	-0.166	57.8
697	ACTGGTACAGTCTCAATAGG	841	61.44	-0.80	0.157	-0.808	-0.210	0.034	341.0
698	CTGGTACAGTCTCAATAGGG	842	63.55	0.10	0.467	-0.025	0.280	0.186	54.8
699	TGGTACAGTCTCAATAGGGC	843	65.89	1.10	0.810	0.844	0.823	0.279	47.1
700	GGTACAGTCTCAATAGGGCT	844	68.08	0.90	1.131	0.670	0.956	0.383	59.7
701	GTACAGTCTCAATAGGGCTA	845	64.73	0.70	0.640	0.496	0.586	0.425	47.0

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
702	TACAGTCTCAATAGGGCTAA	846	59.35	0.70	-0.149	0.496	0.096	0.425	49.3
703	ACAGTCTCAATAGGGCTAAT	847	59.91	0.70	-0.067	0.496	0.147	0.388	55.0
704	CAGTCTCAATAGGGCTAATG	848	59.29	0.70	-0.158	0.496	0.091	0.275	49.0
705	AGTCTCAATAGGGCTAATGG	849	60.62	0.90	0.037	0.670	0.278	0.220	45.7
706	GTCTCAATAGGGCTAATGGG	850	63.00	1.10	0.386	0.844	0.560	0.189	115.6
707	TCTCAATAGGGCTAATGGGA	851	61.22	0.40	0.125	0.236	0.167	0.133	50.6
708	CTCAATAGGGCTAATGGGAA	852	57.97	1.40	-0.352	1.105	0.202	0.075	48.0
709	TCAATAGGGCTAATGGGAAA	853	54.39	1.40	-0.877	1.105	-0.124	-0.028	50.5
710	CAATAGGGCTAATGGGAAAA	854	51.64	1.80	-1.281	1.453	-0.242	-0.194	44.1
711	AATAGGGCTAATGGGAAAAAT	855	50.45	1.90	-1.454	1.540	-0.316	-0.298	43.1
712	ATAGGGCTAATGGGAAAAATT	856	52.34	1.00	-1.178	0.757	-0.442	-0.432	45.2
713	TAGGGCTAATGGGAAAAATT	857	52.63	0.50	-1.135	0.323	-0.581	-0.569	47.4
714	AGGGCTAATGGGAAAAATT	858	52.63	0.50	-1.135	0.323	-0.581	-0.717	50.0
715	GGGCTAATGGGAAAAATT	859	50.89	0.50	-1.390	0.323	-0.739	-0.867	47.8
716	GGCTAATGGGAAAAATT	860	47.14	0.50	-1.940	0.323	-1.080	-1.022	50.2
717	GCTAATGGGAAAAATT	861	45.00	0.50	-2.254	0.323	-1.275	-1.096	43.0
718	CTAATGGGAAAAATT	862	43.95	0.50	-2.408	0.323	-1.371	-1.088	57.0
719	TAATGGGAAAAATT	863	42.27	0.50	-2.655	0.323	-1.524	-1.072	58.7
720	AATGGGAAAAATT	864	46.18	0.70	-2.081	0.496	-1.102	-1.011	183.6
721	ATGGGAAAAATT	865	48.90	1.70	-1.682	1.366	-0.524	-0.924	303.4
722	TGGGAAAAATT	866	47.39	1.80	-1.903	1.453	-0.628	-0.837	135.7
723	GGGAAAAATT	867	47.84	1.60	-1.838	1.279	-0.653	-0.766	241.7
724	GGAAAAATT	868	49.12	1.20	-1.649	0.931	-0.669	-0.737	132.5
725	GAAAAATT	869	48.09	1.20	-1.801	0.931	-0.763	-0.758	128.8
726	AAAAATT	870	45.57	1.10	-2.171	0.844	-1.025	-0.720	141.0
727	AAATTTAAAGTGCACCAAT	871	46.97	1.10	-1.965	0.844	-0.897	-0.679	282.0
728	AATTTAAAGTGCACCAATC	872	49.46	1.10	-1.599	0.844	-0.671	-0.629	948.6

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
729	ATTAAAGTGCAACCAATCT	873	52.84	1.10	-1.104	0.844	-0.363	-0.567	1815.1
730	TTTAAAGTGCAACCAATCTG	874	52.81	1.10	-1.109	0.844	-0.366	-0.426	3188.2
731	TTAAAGTGCAACCAATCTGA	875	53.71	1.00	-0.976	0.757	-0.317	-0.262	3566.1
732	TAAAGTGCAACCAATCTGAG	876	53.56	1.00	-0.999	0.757	-0.331	-0.087	2925.1
733	AAAGTGCAACCAATCTGAGT	877	56.81	1.00	-0.522	0.757	-0.036	0.014	3233.2
734	AAGTGCAACCAATCTGAGTC	878	59.99	1.00	-0.055	0.757	0.254	0.085	3615.6
735	AGTGCAACCAATCTGAGTCA	879	63.25	1.00	0.422	0.757	0.550	0.165	3994.8
736	GTGCAACCAATCTGAGTCAA	880	61.00	1.00	0.093	0.757	0.345	0.138	4033.0
737	TGCAACCAATCTGAGTCAAC	881	58.62	1.00	-0.257	0.757	0.128	0.008	3380.2
738	GCAACCAATCTGAGTCAACA	882	59.87	1.00	-0.073	0.757	0.242	-0.173	4288.7
739	CAACCAATCTGAGTCAACAG	883	56.22	-0.30	-0.608	-0.373	-0.519	-0.445	744.1
740	AACCAATCTGAGTCAACAGA	884	56.24	-1.60	-0.605	-1.504	-0.946	-0.757	392.2
741	ACCAATCTGAGTCAACAGAT	885	58.10	-2.30	-0.332	-2.112	-1.009	-1.030	158.1
742	CCAATCTGAGTCAACAGATT	886	57.90	-3.30	-0.362	-2.982	-1.357	-1.219	70.8
743	CAATCTGAGTCAACAGATTT	887	54.41	-3.80	-0.874	-3.417	-1.840	-1.262	190.0
744	AATCTGAGTCAACAGATTTTC	888	54.37	-3.60	-0.880	-3.243	-1.778	-1.168	87.7
745	ATCTGAGTCAACAGATTTTCT	889	58.37	-2.60	-0.293	-2.373	-1.084	-1.017	152.7
746	TCTGAGTCAACAGATTTCTT	890	58.73	-1.90	-0.241	-1.764	-0.820	-0.797	270.5
747	CTGAGTCAACAGATTTCTTTC	891	58.73	-0.30	-0.241	-0.373	-0.291	-0.553	498.7
748	TGAGTCAACAGATTTCTTCC	892	60.70	0.20	0.049	0.062	0.054	-0.321	891.0
749	GAGTCAACAGATTTCTTCCA	893	62.06	0.20	0.248	0.062	0.177	-0.221	1509.8
750	AGTCAACAGATTTCTTCCAA	894	58.66	0.20	-0.250	0.062	-0.132	-0.182	1009.3
751	GTCAACAGATTTCTTCCAAT	895	58.47	0.20	-0.279	0.062	-0.149	-0.235	1198.0
752	TCAACAGATTTCTTCCAATT	896	55.86	0.20	-0.661	0.062	-0.387	-0.315	680.5
753	CAACAGATTTCTTCCAATTA	897	54.08	0.20	-0.922	0.062	-0.548	-0.381	762.5
754	AACAGATTTCTTCCAATTAT	898	52.82	0.20	-1.107	0.062	-0.663	-0.415	689.8
755	ACAGATTTCTTCCAATTATG	899	54.58	0.20	-0.849	0.062	-0.503	-0.445	715.1

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
756	CAGATTCTTCCAATTATGT	900	56.99	0.20	-0.496	0.062	-0.284	-0.460	833.8
757	AGATTCTTCCAATTATGT	901	56.02	0.20	-0.638	0.062	-0.372	-0.445	1067.7
758	GATTCTTCCAATTATGTG	902	55.80	0.30	-0.670	0.149	-0.359	-0.404	1225.9
759	ATTCTTCCAATTATGTGA	903	55.80	-0.10	-0.670	-0.199	-0.491	-0.382	1028.7
760	TTTCTTCCAATTATGTGAC	904	56.34	-0.10	-0.591	-0.199	-0.442	-0.378	1419.0
761	TTCTTCCAATTATGTGACA	905	57.29	-0.10	-0.452	-0.199	-0.356	-0.348	1437.4
762	TTTCCAATTATGTGACAG	906	57.14	-0.10	-0.474	-0.199	-0.369	-0.325	1518.3
763	CTTCCAATTATGTGACAGG	907	58.36	-0.10	-0.295	-0.199	-0.259	-0.262	1560.3
764	TTCCAATTATGTGACAGGT	908	59.43	-0.10	-0.138	-0.199	-0.161	-0.244	1100.0
765	TCCAATTATGTGACAGGTG	909	59.02	-0.10	-0.198	-0.199	-0.198	-0.246	1096.4
766	CCAATTATGTGACAGGTGT	910	60.68	-0.10	0.046	-0.199	-0.047	-0.424	1103.4
767	CAATTATGTGACAGGTGTA	911	56.24	0.30	-0.605	0.149	-0.319	-0.005	738.1
768	AATTATGTGACAGGTGTAG	912	55.09	1.10	-0.774	0.844	-0.159	0.054	596.7
769	ATTATGTGACAGGTGTAGG	913	59.83	1.10	-0.079	0.844	0.272	0.464	548.1
770	TTATGTGACAGGTGTAGGT	914	63.16	1.10	0.409	0.844	0.575	0.274	701.1
771	TATGTGACAGGTGTAGGTC	915	64.38	-0.20	0.588	-0.286	0.256	0.420	724.7
772	ATGTGACAGGTGTAGGTCC	916	69.08	-0.60	1.278	-0.634	0.551	0.506	1129.8
773	TGTTGACAGGTGTAGGTCCT	917	71.21	-0.60	1.591	-0.634	0.745	0.537	1214.0
774	GTTGACAGGTGTAGGTCCTA	918	70.75	-0.60	1.523	-0.634	0.703	0.520	1425.4
775	TTGACAGGTGTAGGTCCTAC	919	67.83	-0.60	1.095	-0.634	0.438	0.499	838.8
776	TGACAGGTGTAGGTCCTACT	920	69.52	-0.90	1.343	-0.895	0.493	0.427	1173.1
777	GACAGGTGTAGGTCCTACTA	921	69.06	-0.90	1.275	-0.895	0.450	0.304	1367.0
778	ACAGGTGTAGGTCCTACTAA	922	65.30	-0.90	0.723	-0.895	0.108	0.402	872.0
779	CAGGTGTAGGTCCTACTAAT	923	64.69	-0.90	0.634	-0.895	0.053	0.409	897.6
780	AGGTGTAGGTCCTACTAATA	924	62.84	-0.90	0.362	-0.895	-0.115	-0.024	962.2
781	GGTGTAGGTCCTACTAATAC	925	63.19	-0.90	0.414	-0.895	-0.083	-0.090	1382.6
782	GTGTAGGTCCTACTAATACT	926	62.53	-0.90	0.317	-0.895	-0.143	-0.099	1132.9

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _{Mfold} (kcal/mole @ 35 °C)	T _m Score	ΔG _{Mfold} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
783	TGTAGTCTCTACTAATACGT	927	59.27	-0.90	-0.160	-0.895	-0.439	-0.095	1180.7
784	GTAGGTCCTACTAATACGT	928	62.53	-0.50	0.317	-0.547	-0.011	-0.020	1932.9
785	TAGGTCCTACTAATACGT	929	58.77	0.70	-0.234	0.496	0.043	0.042	1634.4
786	AGGTCTCTACTAATACGT	930	59.91	0.50	-0.067	0.323	0.081	0.067	2488.1
787	GGTCTCTACTAATACGT	931	63.54	0.50	0.466	0.323	0.411	0.116	3560.9
788	GTCTCTACTAATACGT	932	62.91	0.50	0.373	0.323	0.354	0.048	3850.1
789	TCCTACTAATACGT	933	59.31	0.50	-0.155	0.323	0.026	-0.041	1879.0
790	CCTACTAATACGT	934	57.99	0.50	-0.348	0.323	-0.093	-0.053	1920.4
791	CTACTAATACGT	935	53.68	0.50	-0.981	0.323	-0.486	-0.094	1131.2
792	TACTAATACGT	936	51.92	0.70	-1.240	0.496	-0.580	-0.147	756.5
793	ACTAATACGT	937	56.45	1.20	-0.574	0.931	-0.002	-0.142	1881.3
794	CTAATACGT	938	57.85	1.20	-0.369	0.931	0.125	-0.102	2033.6
795	TAATACGT	939	56.25	1.20	-0.604	0.931	-0.021	-0.006	1853.9
796	AATACGT	940	57.14	1.20	-0.473	0.931	0.060	0.141	2462.6
797	ATACGT	941	58.55	1.20	-0.266	0.931	0.189	0.183	2436.8
798	TACTGTACCTATAGCTTTATG	942	58.55	1.20	-0.266	0.931	0.189	0.220	1865.2
799	ACTGTACCTATAGCTTTATG	943	59.06	1.20	-0.192	0.931	0.235	0.334	1682.1
800	CTGTACCTATAGCTTTATGT	944	61.64	1.30	0.187	1.018	0.503	0.405	1551.3
801	TGTACCTATAGCTTTATGTC	945	61.08	1.10	0.105	0.844	0.386	0.484	1600.1
802	GTACCTATAGCTTTATGTCC	946	65.16	1.10	0.703	0.844	0.757	0.572	4094.6
803	TACCTATAGCTTTATGTCCA	947	63.16	1.10	0.409	0.844	0.575	0.597	2794.2
804	ACCTATAGCTTTATGTCCAC	948	64.30	1.30	0.577	1.018	0.745	0.575	4754.9
805	CCTATAGCTTTATGTCCACA	949	64.94	1.30	0.671	1.018	0.803	0.554	4185.4
806	CTATAGCTTTATGTCCACAG	950	61.34	1.10	0.143	0.844	0.409	0.484	3284.3
807	TATAGCTTTATGTCCACAGA	951	60.70	1.10	0.048	0.844	0.351	0.453	2819.7
808	ATAGCTTTATGTCCACAGAT	952	61.27	0.60	0.132	0.410	0.238	0.414	3545.1
809	TAGCTTTATGTCCACAGATT	953	61.63	0.60	0.186	0.410	0.271	0.337	4232.6

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG _{Mfold} (kcal/mole @ 35 °C)	T _m Score	ΔG _{Mfold} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
810	AGCTTTATGTCCACAGATTT	954	62.57	0.60	0.324	0.410	0.356	0.283	5252.8
811	GCTTTATGTCCACAGATTC	955	63.85	0.60	0.511	0.410	0.472	0.232	6823.9
812	CTTTATGTCCACAGATTTCT	956	61.56	0.60	0.176	0.410	0.265	0.493	4829.8
813	TTTATGTCCACAGATTTCTA	957	58.97	0.60	-0.205	0.410	0.029	0.473	4333.7
814	TTATGTCCACAGATTTCTAT	958	58.62	0.60	-0.257	0.410	-0.004	0.444	3801.0
815	TATGTCCACAGATTTCTATG	959	58.20	0.60	-0.318	0.410	-0.041	0.442	3528.2
816	ATGTCCACAGATTTCTATGA	960	60.12	0.60	-0.036	0.410	0.134	0.429	2080.0
817	TGTCCACAGATTTCTATGAG	961	60.34	0.60	-0.004	0.410	0.153	0.445	913.8
818	GTCACACAGATTTCTATGAGT	962	63.68	0.60	0.486	0.410	0.457	0.422	1228.3
819	TCCACAGATTTCTATGAGTA	963	59.83	0.80	-0.078	0.583	0.173	0.067	238.1
820	CCACAGATTTCTATGAGTAT	964	58.43	1.10	-0.285	0.844	0.144	-0.078	219.4
821	CACAGATTTCTATGAGTATC	965	55.78	0.90	-0.673	0.670	-0.162	-0.469	138.6
822	ACAGATTTCTATGAGTATCT	966	56.48	-0.10	-0.571	-0.199	-0.430	-0.273	112.7
823	CAGATTTCTATGAGTATCTG	967	55.85	-1.30	-0.663	-1.243	-0.883	-0.327	133.8
824	AGATTTCTATGAGTATCTGA	968	55.87	-0.10	-0.659	-0.199	-0.485	-0.387	296.8
825	GATTTCTATGAGTATCTGAT	969	55.69	0.60	-0.686	0.410	-0.270	-0.442	279.7
826	ATTCTATGAGTATCTGATC	970	55.67	0.80	-0.689	0.583	-0.206	-0.498	484.4
827	TTTCTATGAGTATCTGATCA	971	57.06	0.20	-0.485	0.062	-0.277	-0.540	502.0
828	TTCTATGAGTATCTGATCAT	972	56.70	-0.50	-0.538	-0.547	-0.541	-0.569	637.3
829	TCTATGAGTATCTGATCATA	973	55.75	-1.10	-0.678	-1.069	-0.826	-0.667	489.0
830	CTATGAGTATCTGATCATAC	974	54.95	-1.30	-0.794	-1.243	-0.965	-0.742	808.7
831	TATGAGTATCTGATCATACT	975	54.95	-1.10	-0.794	-1.069	-0.899	-0.738	903.2
832	ATGAGTATCTGATCATACTG	976	55.49	-1.20	-0.715	-1.156	-0.883	-0.707	1709.3
833	TGAGTATCTGATCATACTGT	977	58.64	-1.20	-0.254	-1.156	-0.597	-0.604	2103.9
834	GAGTATCTGATCATACTGTC	978	60.20	-1.20	-0.025	-1.156	-0.455	-0.468	3973.4
835	AGTATCTGATCATACTGTCT	979	60.88	-1.00	0.076	-0.982	-0.326	-0.330	6462.3
836	GTATCTGATCATACTGTCTT	980	61.03	-0.30	0.097	-0.373	-0.081	-0.167	9749.0

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
837	TATCTGATCATACGTCTTGA	981	57.16	0.90	-0.470	0.670	-0.037	-0.059	7817.2
838	ATCTGATCATACGTCTTAC	982	58.34	0.90	-0.298	0.670	0.070	0.007	9683.1
839	TCTGATCATACGTCTTACT	983	60.42	0.90	0.008	0.670	0.259	0.055	8089.0
840	CTGATCATACGTCTTACTT	984	59.32	0.90	-0.154	0.670	0.159	0.067	8696.8
841	TGATCATACGTCTTACTTT	985	57.63	0.90	-0.401	0.670	0.006	0.064	6880.5
842	GATCATACGTCTTACTTTG	986	57.63	0.90	-0.401	0.670	0.006	0.020	7033.7
843	ATCATACGTCTTACTTTGA	987	57.63	0.90	-0.401	0.670	0.006	-0.093	5406.5
844	TCATACGTCTTACTTTGAT	988	57.63	0.70	-0.401	0.496	-0.060	-0.215	4239.4
845	CATACGTCTTACTTTGATA	989	55.68	0.70	-0.688	0.496	-0.238	-0.378	3727.4
846	ATACTGTCTTACTTTGATAA	990	52.44	0.70	-1.163	0.496	-0.533	-0.550	2665.5
847	TACTGTCTTACTTTGATAAA	991	50.65	0.70	-1.426	0.496	-0.696	-0.696	1817.8
848	ACTGTCTTACTTTGATAAAA	992	49.49	-0.30	-1.595	-0.373	-1.131	-0.809	1335.9
849	CTGTCTTACTTTGATAAAC	993	49.49	-0.50	-1.595	-0.547	-1.197	-0.916	1526.2
850	TGCTTACTTTGATAAACCC	994	51.45	-0.50	-1.309	-0.547	-1.019	-0.949	822.7
851	GTCTTACTTTGATAAACCT	995	53.32	-0.50	-1.034	-0.547	-0.849	-0.966	1227.4
852	TCTTACTTTGATAAACCTC	996	51.75	-0.50	-1.264	-0.547	-0.991	-0.946	503.0
853	CTTACTTTGATAAACCTCC	997	54.28	-0.50	-0.894	-0.547	-0.762	-0.910	1174.3
854	TTACTTTGATAAACCTCCA	998	53.70	-0.50	-0.978	-0.547	-0.814	-0.901	885.5
855	TACTTTGATAAACCTCCAA	999	51.79	-0.50	-1.259	-0.547	-0.988	-0.916	650.6
856	ACTTTGATAAACCTCCAAT	1000	52.29	-0.50	-1.185	-0.547	-0.943	-0.826	615.4
857	CTTTGATAAACCTCCAATT	1001	52.11	-0.50	-1.212	-0.547	-0.959	-0.728	563.4
858	TTTGATAAACCTCCAATTC	1002	51.46	-0.30	-1.307	-0.373	-0.952	-0.561	420.9
859	TTGATAAACCTCCAATTCC	1003	54.68	0.60	-0.834	0.410	-0.362	-0.298	536.6
860	TGATAAACCTCCAATCCCC	1004	57.79	0.60	-0.378	0.410	-0.079	-0.022	1417.8
861	GATAAACCTCCAATCCCC	1005	61.15	1.00	0.114	0.757	0.359	0.258	4351.2
862	ATAAACCTCCAATCCCCC	1006	63.24	1.90	0.421	1.540	0.846	0.560	7738.7
863	TAAACCTCCAATCCCCCT	1007	64.88	1.90	0.663	1.540	0.996	0.817	11136.0

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{Mfold} (kcal/mole @ 35 °C)	T _m Score	ΔG_{Mfold} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
864	AAACCTCCAAATCCCCCTA	1008	64.88	1.90	0.663	1.540	0.996	1.074	14811.0
865	AAACCTCCAAATCCCCCTAT	1009	66.73	1.90	0.933	1.540	1.164	1.261	15751.0
866	AACCTCCAAATCCCCCTATC	1010	70.07	1.80	1.424	1.453	1.435	1.330	19661.0
867	ACCTCCAAATCCCCCTATCA	1011	73.21	1.80	1.883	1.453	1.720	1.335	20301.0
868	CCTCCAAATCCCCCTATCAT	1012	72.64	1.80	1.801	1.453	1.669	1.327	19376.0
869	CTCCAAATCCCCCTATCATT	1013	69.66	1.60	1.364	1.279	1.332	1.254	17642.0
870	TCGAATCCCCCTATCATTT	1014	68.21	1.10	1.150	0.844	1.034	1.093	13751.0
871	CGAATCCCCCTATCATTTT	1015	67.12	1.10	0.991	0.844	0.935	0.931	12669.0
872	CAATCCCCCTATCATTTT	1016	64.02	1.10	0.536	0.844	0.653	0.848	9255.9
873	AATCCCCCTATCATTTTG	1017	62.80	0.40	0.357	0.236	0.311	0.753	8929.1
874	ATCCCCCTATCATTTTGG	1018	67.28	0.00	1.014	-0.112	0.586	0.745	6148.2
875	TTCCCCCTATCATTTTGGT	1019	70.46	0.00	1.480	-0.112	0.875	0.664	5468.0
876	TCCCCCTATCATTTTGGTT	1020	70.46	0.00	1.480	-0.112	0.875	0.653	5803.7
877	CCCCCTATCATTTTGGTTT	1021	69.27	0.00	1.307	-0.112	0.768	0.658	5192.0
878	CCCTATCATTTTGGTTTC	1022	67.18	0.00	1.000	-0.112	0.577	0.549	3557.4
879	CCCTATCATTTTGGTTCC	1023	67.18	0.00	1.000	-0.112	0.577	0.392	5274.3
880	CTATCATTTTGGTTTCCA	1024	64.63	0.00	0.625	-0.112	0.345	0.270	3787.9
881	CTATCATTTTGGTTTCCAT	1025	60.77	-0.50	0.059	-0.547	-0.171	0.467	2726.8
882	TATCATTTTGGTTTCCATC	1026	60.20	-0.50	-0.025	-0.547	-0.223	0.002	3249.9
883	ATCATTTTGGTTTCCATCT	1027	62.83	-0.50	0.361	-0.547	0.016	0.051	5548.9
884	TCATTTTGGTTTCCATCTT	1028	63.21	-0.50	0.416	-0.547	0.050	0.071	5290.0
885	CATTTTGGTTTCCATCTTC	1029	63.21	-0.50	0.416	-0.547	0.050	0.457	7451.0
886	ATTTTGGTTTCCATCTCCT	1030	65.88	-0.50	0.809	-0.547	0.293	0.262	11578.0
887	TTTTGGTTTCCATCTCCTG	1031	67.93	-0.50	1.109	-0.547	0.480	0.366	13722.0
888	TTTGGTTTCCATCTCCTGG	1032	67.42	-0.50	1.035	-0.547	0.434	0.475	15064.0
889	TTGGTTTCCATCTCCTGG	1033	69.71	-0.90	1.370	-0.895	0.509	0.554	10869.0
890	TTGGTTTCCATCTCCTGGC	1034	73.74	-1.30	1.962	-1.243	0.744	0.535	16035.0

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
891	TGTTTCCATCTTCTGGCA	1035	74.48	-1.30	2.071	-1.243	0.812	0.457	16304.0
892	GGTTTCCATCTTCTGGCAA	1036	72.21	-1.30	1.737	-1.243	0.605	0.406	14885.0
893	GTTTCCATCTTCTGGCAA	1037	67.37	-1.30	1.027	-1.243	0.165	0.358	11910.0
894	TTTCCATCTTCTGGCAAAC	1038	64.82	-1.30	0.653	-1.243	-0.067	0.290	11929.0
895	TTCCATCTTCTGGCAAAC	1039	66.34	-1.30	0.877	-1.243	0.071	0.252	11517.0
896	TCCATCTTCTGGCAAAC	1040	67.47	-1.30	1.042	-1.243	0.174	0.237	11822.0
897	CCATCTTCTGGCAAAC	1041	67.12	-0.90	0.991	-0.895	0.274	0.285	11710.0
898	CATCTTCTGGCAAAC	1042	63.55	0.90	0.466	0.670	0.544	0.357	7635.3
899	ATCTTCTGGCAAAC	1043	62.71	1.00	0.343	0.757	0.501	0.409	8378.2
900	TCTTCTGGCAAAC	1044	63.06	0.90	0.395	0.670	0.500	0.446	6321.4
901	CTTCTGGCAAAC	1045	63.06	0.70	0.395	0.496	0.434	0.468	7659.0
902	TTCTGGCAAAC	1046	63.06	0.70	0.395	0.496	0.434	0.429	11621.0
903	TCCTGGCAAAC	1047	63.06	0.70	0.395	0.496	0.434	0.363	3389.0
904	CCTGGCAAAC	1048	63.06	0.70	0.395	0.496	0.434	0.273	3870.6
905	CTGGCAAAC	1049	61.24	0.70	0.127	0.496	0.268	0.160	1992.7
906	TGGCAAAC	1050	58.74	0.70	-0.239	0.496	0.040	-0.045	698.3
907	GGCAAAC	1051	56.86	0.70	-0.514	0.496	-0.130	-0.204	718.3
908	GCAAAC	1052	54.36	0.70	-0.882	0.496	-0.358	-0.339	372.3
909	CAAACT	1053	49.93	0.60	-1.530	0.410	-0.793	-0.430	180.6
910	AACT	1054	49.11	0.60	-1.651	0.410	-0.868	-0.455	430.0
911	ACT	1055	52.79	0.60	-1.111	0.410	-0.533	-0.494	904.3
912	CTCT	1056	54.63	0.60	-0.842	0.410	-0.366	-0.540	1663.5
913	CTCTCT	1057	57.14	0.60	-0.474	0.410	-0.138	-0.459	2694.2
914	CTCTCTCT	1058	54.51	0.60	-0.859	0.410	-0.377	-0.364	3222.9
915	CTCTCTCTCT	1059	53.21	0.60	-1.049	0.410	-0.495	-0.340	3142.8
916	CTCTCTCTCTCT	1060	53.13	0.80	-1.061	0.583	-0.436	-0.270	5867.0
917	CTCTCTCTCTCTCT	1061	54.51	1.20	-0.859	0.931	-0.179	-0.253	6641.4

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
918	TTCTTCTAATACTGTATCAT	1062	54.17	1.30	-0.908	1.018	-0.176	-0.229	7151.9
919	TCTTCTAATACTGTATCATC	1063	55.17	1.30	-0.762	1.018	-0.086	-0.439	8134.9
920	CTTCTAATACTGTATCATCT	1064	55.86	1.30	-0.661	1.018	-0.023	-0.048	8551.4
921	TTCTAATACTGTATCATCTG	1065	53.80	1.30	-0.964	1.018	-0.211	-0.003	5741.7
922	TCTAATACTGTATCATCTGC	1066	57.65	1.30	-0.398	1.018	0.140	0.404	8575.9
923	CTAATACTGTATCATCTGCT	1067	58.28	1.30	-0.307	1.018	0.197	0.248	8980.3
924	TAATACTGTATCATCTGCTC	1068	57.65	1.30	-0.398	1.018	0.140	0.384	10762.0
925	AATACTGTATCATCTGCTCC	1069	62.19	1.30	0.268	1.018	0.553	0.566	17037.0
926	ATACTGTATCATCTGCTCCT	1070	66.43	1.30	0.889	1.018	0.938	0.682	20970.0
927	TACTGTATCATCTGCTCCTG	1071	66.32	1.30	0.874	1.018	0.929	0.763	23084.0
928	ACTGTATCATCTGCTCCTGT	1072	70.36	0.60	1.466	0.410	1.065	0.875	24474.0
929	CTGTATCATCTGCTCCTGTA	1073	69.13	0.60	1.286	0.410	0.953	0.910	22217.0
930	TGTATCATCTGCTCCTGTAT	1074	67.04	0.60	0.979	0.410	0.763	0.890	19829.0
931	GTATCATCTGCTCCTGTATC	1075	68.85	0.60	1.244	0.410	0.927	0.842	23548.0
932	TATCATCTGCTCCTGTATCT	1076	67.44	0.60	1.037	0.410	0.799	0.773	21759.0
933	ATCATCTGCTCCTGTATCTA	1077	67.44	0.60	1.037	0.410	0.799	0.725	22711.0
934	TCACTGCTCCTGTATCTAA	1078	65.13	0.60	0.699	0.410	0.589	0.706	18134.0
935	CATCTGCTCCTGTATCTAAT	1079	63.60	1.00	0.475	0.757	0.582	0.644	17772.0
936	ATCTGCTCCTGTATCTAATA	1080	61.77	1.60	0.207	1.279	0.614	0.502	17134.0
937	TCTGCTCCTGTATCTAATAG	1081	62.01	1.60	0.241	1.279	0.635	0.389	10969.0
938	CTGCTCCTGTATCTAATAGA	1082	61.90	0.50	0.225	0.323	0.262	0.336	9556.3
939	TGCTCCTGTATCTAATAGAG	1083	60.12	0.30	-0.036	0.149	0.034	0.264	3739.9
940	GCTCCTGTATCTAATAGAGC	1084	64.50	-1.00	0.607	-0.982	0.003	0.487	4088.3
941	CTCCTGTATCTAATAGAGCT	1085	62.21	0.30	0.271	0.149	0.224	0.406	2263.0
942	TCTGTATCTAATAGAGCTT	1086	60.56	0.30	0.028	0.149	0.074	0.080	1018.0
943	CCTGTATCTAATAGAGCTTC	1087	60.56	0.30	0.028	0.149	0.074	0.004	1319.1
944	CTGTATCTAATAGAGCTTCC	1088	60.56	0.30	0.028	0.149	0.074	0.070	2347.8

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
945	GTATCTAATAGAGCTTCCT	1089	60.56	0.30	0.028	0.149	0.074	0.048	1871.6
946	GTATCTAATAGAGCTTCCTT	1090	61.00	0.30	0.092	0.149	0.114	-0.040	3469.1
947	TATCTAATAGAGCTTCCTTT	1091	58.20	0.30	-0.318	0.149	-0.141	-0.030	1114.6
948	ATCTAATAGAGCTTCCTTA	1092	58.20	0.30	-0.318	0.149	-0.141	-0.057	1358.4
949	TCTAATAGAGCTTCCTTAG	1093	58.39	0.30	-0.289	0.149	-0.123	-0.078	665.4
950	CTAATAGAGCTTCCTTAGT	1094	60.12	0.00	-0.036	-0.112	-0.065	-0.049	807.4
951	TAATAGAGCTTCCTTAGTT	1095	58.46	0.30	-0.280	0.149	-0.117	0.428	608.7
952	AATAGAGCTTCCTTTAGTTG	1096	58.97	0.30	-0.205	0.149	-0.070	0.332	623.8
953	ATAGAGCTTCCTTTAGTTGC	1097	65.53	0.30	0.758	0.149	0.526	0.576	674.5
954	TAGAGCTTCCTTTAGTTGCC	1098	69.50	0.30	1.340	0.149	0.887	0.841	814.3
955	AGAGCTTCCTTTAGTTGCC	1099	73.89	0.30	1.983	0.149	1.286	1.157	1183.8
956	GAGCTTCCTTTAGTTGCC	1100	77.20	0.30	2.470	0.149	1.588	1.454	2219.4
957	AGCTTCCTTTAGTTGCC	1101	79.38	0.30	2.789	0.149	1.785	1.650	4642.2
958	GCTTCCTTTAGTTGCC	1102	82.41	0.40	3.234	0.236	2.095	1.765	8804.8
959	CTTCCTTTAGTTGCC	1103	80.06	0.80	2.889	0.583	2.013	1.823	11331.0
960	TTCCCTTTAGTTGCC	1104	77.67	1.10	2.539	0.844	1.895	1.818	12976.0
961	TCCTTTAGTTGCC	1105	77.27	0.60	2.480	0.410	1.693	1.765	12369.0
962	CCTTAGTTGCC	1106	77.27	0.60	2.480	0.410	1.693	1.669	15090.0
963	CTTAGTTGCC	1107	75.74	0.60	2.255	0.410	1.554	1.581	16130.0
964	TTTAGTTGCC	1108	74.23	0.60	2.033	0.410	1.416	1.545	15304.0
965	TTAGTTGCC	1109	74.23	0.60	2.033	0.410	1.416	1.539	14829.0
966	TAGTTGCC	1110	73.31	0.80	1.899	0.583	1.399	1.490	15309.0
967	AGTGCCCCCTATCTTAT	1111	73.83	1.40	1.976	1.105	1.645	1.498	15205.0
968	GTGCCCCCTATCTTATT	1112	73.91	1.40	1.986	1.105	1.652	1.524	14192.0
969	TTGCCCCCTATCTTATTG	1113	70.59	1.40	1.500	1.105	1.350	1.515	8699.5
970	TGCCCCCTATCTTATTGT	1114	73.39	1.40	1.911	1.105	1.605	1.461	7786.6
971	GCCTCCCCCTATCTTATTGTG	1115	73.39	1.40	1.911	1.105	1.605	1.328	6709.1

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
972	CCCCCTATCTTTATTGTGA	1116	70.61	1.40	1.502	1.105	1.351	1.165	6198.4
973	CCCCCTATCTTTATTGTGAC	1117	67.66	1.20	1.070	0.931	1.017	0.999	4910.2
974	CCCCCTATCTTTATTGTGACG	1118	64.37	1.20	0.587	0.931	0.718	0.780	850.0
975	CCCCCTATCTTTATTGTGACGA	1119	62.05	1.20	0.248	0.931	0.507	0.570	404.9
976	CCTATCTTTATTGTGACGAG	1120	58.56	1.20	-0.265	0.931	0.190	0.436	166.6
977	CTATCTTTATTGTGACGAGG	1121	57.28	1.20	-0.452	0.931	0.073	0.376	126.9
978	TATCTTTATTGTGACGAGGG	1122	57.91	1.20	-0.361	0.931	0.130	0.279	92.6
979	ATCTTTATTGTGACGAGGGG	1123	61.03	1.20	0.097	0.931	0.414	0.473	97.9
980	TCTTTATTGTGACGAGGGGT	1124	64.18	0.90	0.559	0.670	0.601	0.007	122.3
981	CTTTATTGTGACGAGGGTC	1125	64.18	-0.80	0.559	-0.808	0.039	0.013	267.0
982	TTTATTGTGACGAGGGTCG	1126	62.63	-1.20	0.332	-1.156	-0.233	-0.073	396.0
983	TTATTGTGACGAGGGTCGT	1127	65.37	-2.30	0.734	-2.112	-0.348	-0.145	446.0
984	TATTGTGACGAGGGTCGTT	1128	65.37	-2.80	0.734	-2.547	-0.513	-0.202	661.9
985	ATTGTGACGAGGGTCGTTG	1129	65.82	-2.80	0.800	-2.547	-0.472	-0.163	864.5
986	TTGTGACGAGGGTCGTTGC	1130	70.01	-2.80	1.414	-2.547	-0.091	-0.156	1465.7
987	TGTGACGAGGGTCGTTGCC	1131	73.21	-2.80	1.884	-2.547	0.200	-0.157	2836.9
988	GTGACGAGGGTCGTTGCCA	1132	74.44	-2.80	2.065	-2.547	0.312	-0.137	3589.7
989	TGACGAGGGTCGTTGCCAA	1133	69.05	-2.80	1.274	-2.547	-0.178	-0.058	2100.4
990	GACGAGGGTCGTTGCCAAA	1134	67.10	-2.80	0.988	-2.547	-0.355	0.042	1948.7
991	ACGAGGGTCGTTGCCAAAG	1135	66.13	-2.60	0.845	-2.373	-0.378	0.425	1384.3
992	CGAGGGTCGTTGCCAAAGA	1136	66.81	-1.40	0.945	-1.330	0.081	0.487	1192.0
993	GAGGGTCGTTGCCAAAGAG	1137	66.84	0.20	0.950	0.062	0.612	0.304	1221.0
994	AGGGTCGTTGCCAAAGAGT	1138	68.70	0.20	1.223	0.062	0.782	0.427	953.2
995	GGGTCGTTGCCAAAGAGTG	1139	68.32	0.20	1.167	0.062	0.747	0.515	988.6
996	GGTCGTTGCCAAAGAGTGA	1140	67.11	0.20	0.989	0.062	0.636	0.476	937.8
997	GGTCGTTGCCAAAGAGTGAT	1141	64.59	0.50	0.620	0.323	0.507	0.333	852.1
998	GTCGTTGCCAAAGAGTGATC	1142	63.51	0.00	0.461	-0.112	0.243	0.176	1189.4

Table 4

p5 Probe Position	DNA Probe Sequence	SEQ ID NO:	RNA/DNA T _m (°C)	ΔG_{MFOLD} (kcal/mole @ 35 °C)	T _m Score	ΔG_{MFOLD} Score	Composite Score	Window-Averaged Composite Score	HIV PRT GeneChip™ Data
999	TCGTTGCCAAAGAGTGATCT	1143	62.35	-1.00	0.291	-0.982	-0.192	-0.042	1501.7
1000	CGTTGCCAAAGAGTGATCTG	1144	60.92	-1.20	0.081	-1.156	-0.389	-0.456	1360.9
1001	GTTCGCAAGAGTGATCTGA	1145	61.71	-1.20	0.198	-1.156	-0.317	-0.263	1112.9
1002	TTGCCAAAGAGTGATCTGAG	1146	58.90	-1.20	-0.215	-1.156	-0.572	-0.353	468.3
1003	TGCCAAAGAGTGATCTGAGG	1147	61.08	-1.20	0.104	-1.156	-0.375	-0.454	400.1
1004	GCCAAAGAGTGATCTGAGGG	1148	63.68	-1.50	0.485	-1.417	-0.237	-0.544	401.6
1005	CCAAAGAGTGATCTGAGGGA	1149	60.94	-1.20	0.084	-1.156	-0.387	-0.575	199.9
1006	CAAGAGTGATCTGAGGGAA	1150	55.32	-1.20	-0.741	-1.156	-0.899	-0.530	202.1
1007	AAAGAGTGATCTGAGGGAAG	1151	54.21	-1.20	-0.903	-1.156	-0.999	-0.494	258.7
1008	AAGAGTGATCTGAGGGAAGT	1152	59.12	-1.20	-0.183	-1.156	-0.552	-0.475	274.7
1009	AGAGTGATCTGAGGGAAGTT	1153	61.60	-1.00	0.181	-0.982	-0.261	-0.463	297.2
1010	GAGTGATCTGAGGGAAGTTA	1154	60.78	-0.30	0.061	-0.373	-0.104	-0.414	250.6
1011	AGTGATCTGAGGGAAGTTAA	1155	57.35	0.60	-0.443	0.410	-0.119	-0.348	231.3
1012	GTGATCTGAGGGAAGTTAAA	1156	55.25	0.60	-0.751	0.410	-0.310	-0.286	214.5
1013	TGATCTGAGGGAAGTTAAAG	1157	52.55	0.60	-1.147	0.410	-0.556	-0.295	102.3
1014	GATCTGAGGGAAGTTAAAGG	1158	55.09	0.60	-0.774	0.410	-0.324	-0.330	102.3
1015	ATCTGAGGGAAGTTAAAGGA	1159	55.09	0.60	-0.774	0.410	-0.324	-0.367	49.4
1016	CTGAGGGAAGTTAAAGGAT	1160	55.09	0.60	-0.774	0.410	-0.324	-0.379	104.3
1017	CTGAGGGAAGTTAAAGGATA	1161	53.32	1.00	-1.034	0.757	-0.353	-0.370	46.3
1018	TGAGGGAAGTTAAAGGATAC	1162	51.95	1.30	-1.235	1.018	-0.378	-0.360	50.9
1019	GAGGGAAGTTAAAGGATACA	1163	53.26	0.90	-1.043	0.670	-0.392		58.2
1020	AGGGAAGTTAAAGGATACAG	1164	52.14	0.90	-1.207	0.670	-0.494		50.5
1021	GGGAAGTTAAAGGATACAGT	1165	54.81	0.90	-0.815	0.670	-0.251		53.1

Example 3

Synopsis: The method of the present invention is particularly useful as a guide to the iterative refinement of probes. One of the specific predictions made for rabbit β -globin in Example 1 is used to provide an example of such a refinement.

Materials and Methods: The contig spanning positions 5-11 of a portion of the rabbit β -globin gene (Example 1, Table 3) was analyzed, using the experimentally measured data to simulate the results of successive experimental measurements.

The iterative refinement was performed using a rule-based algorithm, outlined below. This algorithm is used by way of example only; other algorithms for efficiently finding local maxima are well known to the art and could be employed to perform this task.

Given experimental data for probes from the 1st quartile, median and 3rd quartile of a contig, as well as a user-set signal threshold for further consideration of a probe,

- 1) If all 3 measurements are below the user-specified signal threshold, discard the prediction.
- 2) If at least one of the measurements is above the user-specified threshold, determine which point yields the maximum signal.
 - a) If the maximum point is the 1st quartile probe, then make three new measurements for probes with the same spacing as that used in the preceding iteration, but displaced so that the third probe is identical to the original 1st quartile probe. In other words, repeat the search with the same pattern and spacing, but displace the pattern in the direction of increasing signal found in the first experiment.
 - b) If the maximum point is the 3rd quartile probe, then make three new measurements for probes with the same spacing as that used in the preceding iteration, but displaced so that the first probe is identical to the original 3rd quartile probe. In other words, repeat the search with the same

pattern and spacing, but displace the pattern in the direction of increasing signal found in the first experiment.

- c) If the maximum point is the median probe, then repeat the experiment, keeping the median point the same, but shrinking the spacing between probes by a factor of 2.

- 3) Continue iteration until a maximum is found, or the user judges the signal level observed to be acceptable. Use the experimental value measured for the probe duplicated in successive iterations to tie together the successive data sets, via a simple normalization procedure, described below. Where appropriate, consider all of the data (i.e. all of the iterations) when deciding how to proceed, or whether the peak hybridization intensity has been found.

Results: Iterative refinement of the contig spanning positions 5-11 in Table 3 proceeds as follows:

Iteration 1: Probes are synthesized at positions 6, 8 and 10, yielding the experimental hybridization intensities 180, 220 and 310, respectively.

Iteration 2: Following rule 2b), probes are synthesized at positions 10, 12 and 14.

Note that the redundant measurement at position 10 serves as a bridge between experiments, and allows comparison of the two sets by normalizing the intensities by multiplying the second iteration measurements by the ratio of the intensity observed for the probe at position 10 in the first iteration to the value observed in the second iteration. In the simplest case, the ratio is 1; in any case, the second iteration yields the normalized values 310, 390, 240 for probe positions 10, 12 and 14, respectively.

Iteration 3: By rule 2c), measurements are performed for probes at positions 11, 12 and 13; after normalization, these yield the normalized hybridization intensities 320, 390 and 410, respectively. Combination of these results with the results from iteration 2, probe position 14, yields the conclusion that the best probe for this intensity peak is the probe that starts at sequence position 13.

The overall result is that iterative improvement converges in three iterations, and requires the synthesis of seven test probes, one of which is the local optimal probe. In addition, the first and second iterations yield probes that exhibit 75% and 95% of the local maximum hybridization intensities, respectively. In many applications, either of these probes would be considered acceptable.

The above examples 1 and 2 demonstrate that two different implementations of the method of the present invention are capable of efficiently predicting regions of high hybridization efficiency in a variety of polynucleotide targets. Many of the predictions yield acceptable probe sequences on the first design iteration, and all would yield optimized probe sets after 2-4 rounds of iterative refinement, as demonstrated in Example 3. The performance demonstrated in these examples greatly exceeds the performance of current methods. Finally, the examples demonstrate that the predictions can be performed by a software application that has been implemented and installed on a Pentium®-based computer workstation.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shannon, Karen W.
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Webb, Peter G.
Kincaid, Robert H.
- (ii) TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences
- (iii) NUMBER OF SEQUENCES: 1165
- (iv) CORRESPONDENCE ADDRESS:
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(E) COUNTRY: USA
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Not available
(B) FILING DATE: 10-FEB-1998
(C) CLASSIFICATION: Not available
- (viii) ATTORNEY/AGENT INFORMATION:
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(B) TELEFAX: 650-852-8063

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(ix) FEATURE:
 (A) NAME/KEY: stem_loop
 (B) LOCATION: 2..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTGGCAATC ACAATTGCCA GTAA

24

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: tRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:
 (A) NAME/KEY: tRNA
 (B) LOCATION: 1..75
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /function= "transfer RNA"
/product= "tRNA-Ala"
/evidence= EXPERIMENTAL
/anticodon= (pos: 34 .. 36, aa: Ala)
/citation= ([1][2])

(ix) FEATURE:
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 (B) LOCATION: 9
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/frequency= 0.9999
/mod_base= mlg
/citation= ([1][2])

(ix) FEATURE:
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 (B) LOCATION: 16
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/frequency= 0.9999
/mod_base= d
/citation= ([1][2])

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 20
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/frequency= 0.9999
/mod_base= d
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 26
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/frequency= 0.9999
/mod_base= m22g
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 34
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/frequency= 0.9999
/mod_base= i
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 37
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/frequency= 0.9999
/mod_base= mli
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 38
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/frequency= 0.9999
/mod_base= p
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 46
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/frequency= 0.9999
/mod_base= d
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 53
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/frequency= 0.9999
/mod_base= t
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified_base

(B) LOCATION: 54
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/frequency= 0.9999
/mod_base= p
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Holley, R. W.
Apgar, J.
Everett, G. A.
Madison, J. T.
Marquisee, M.
Merrill, S. H.
Penswick, J. R.
Zamir, A.
(B) TITLE: Structure of a ribonucleic acid
(C) JOURNAL: Science
(D) VOLUME: 147
(F) PAGES: 1462-1465
(G) DATE: 1965
(K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 75

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Penswick, J. R.
Martin, R.
Dirheimer, G.
(B) TITLE: Evidence supporting a revised sequence for
yeast alanine tRNA
(C) JOURNAL: FEBS Lett.
(D) VOLUME: 50
(F) PAGES: 28-31
(G) DATE: 1975
(K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGCGUGUGG CGUAGUCGGU AGCGCGCUCC CUUGGCGUGG GAGAGUCUCC GGUUCGAUUC 60
CGGACUCGUC CACCA 75

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

0971464-02460

ATGGACTTAG CATTCG

16

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGGACTTAG CA

12

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGGACTTAGC AT

12

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGACTTAGCA TT

12

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GACTTAGCAT TC

12

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACTTAGCATT CG

12

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GTCCAAAAG GGTCACTCTA CCTCCGCCA TAAAAACTC ATGTTCAAGA

50

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTCCAAAAG GGTCACTCTA CCTCC

25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCCAAAAGG GTCAGTCTAC CTCCC

25

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCAAAAAGGG TCAGTCTACC TCCCG

25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CAAAAAGGGT CAGTCTACCT CCCGC

25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AAAAAGGGTC AGTCTACCTC CCGCC

25

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

0971464-021504

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

AAAAGGGTCA GTCTACCTCC CGCCA

25

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AAAGGGTCAG TCTACCTCCC GCCAT

25

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGGGTCAGT CTACCTCCCG CCATA

25

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AGGGTCAGTC TACCTCCCGC CATAA

25

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGGTCAGTCT ACCTCCCGCC ATAAA

25

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGTCAGTCTA CCTCCCGCCA TAAAA

25

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GTCACTCTAC CTCCCGCCAT AAAAA

25

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCAGTCTACC TCCCGCCATA AAAAA

25

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CAGTCTACCT CCCGCCATAA AAAAC

25

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AGTCTACCTC CCGCCATAAA AACT

25

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GTCTACCTCC CGCCATAAAA AACTC

25

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TCTACCTCCC GCCATAAAAA ACTCA

25

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CTACCTCCCG CCATAAAAAA CTCAT

25

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TACCTCCCGC CATAAAAAAC TCATG

25

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

10971464-10310

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ACCTCCCGCC ATAAAAA ACT CATGT

25

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CCTCCCGCCA TAAAAA ACTC ATGTT

25

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CTCCCGCCAT AAAAAA CTCA TGTTC

25

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TCCCGCCATA AAAAATCAT GTTCA

25

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCCGCCATAA AAAAATCATG TTCAA

25

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CCGCCATAAA AAATCATGT TCAAG

25

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGCCATAAAA AACTCATGTT CAAGA

25

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Oryctolagus cuniculus*
 - (ix) FEATURE:
 - (A) NAME/KEY: 5'UTR
 - (B) LOCATION: 1..53
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 54..122
 - (D) OTHER INFORMATION: /codon_start= 54
- /product= "rabbit betal globin, N-terminus"
- /citation= ([1])
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Rohrbaugh, M. L.
III Johnson, J. E.
James, M. D.
Hardison, R. C.
 - (B) TITLE: Transcriptional unit of the rabbit betal
globin gene
 - (C) JOURNAL: Mol. Cell. Biol.
 - (D) VOLUME: 5
 - (F) PAGES: 147-160
 - (G) DATE: 1985
 - (K) RELEVANT RESIDUES IN SEQ ID NO: 36: FROM 1 TO 122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ACACTTGCTT TTGACACAAC TGTGTTTACT TGCAATCCCC CAAAACAGAC AGA ATG

56

Met
1

GTG CAT CTG TCC AGT GAG GAG AAG TCT GCG GTC ACT GCC CTG TGG GGC 104
Val His Leu Ser Ser Glu Glu Lys Ser Ala Val Thr Ala Leu Trp Gly
5 10 15

AAG GTG AAT GTG GAA GAA 122
Lys Val Asn Val Glu Glu
20

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human immunodeficiency virus
- (B) STRAIN: type I
- (C) INDIVIDUAL ISOLATE: BH10

(ix) FEATURE:

- (A) NAME/KEY: misc_RNA
- (B) LOCATION: 1..1040
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /partial

/function= "protease & reverse transcriptase
regions"
/product= "pol polyprotein (partial)"
/evidence= EXPERIMENTAL
/citation= ([1])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Wong-Stahl, F.
Gallo, R. C.
Chang, N. T.
Ghrayeb, J.
Papas, T. S.
Lautenberger, J. A.
Pearson, M. L.
Jr. Petteway, S. R.
Ivanoff, L.
Baumeister, K.
- (B) TITLE: Complete nucleotide sequence of the AIDS
virus, HTLV-III
- (C) JOURNAL: Nature
- (D) VOLUME: 313
- (F) PAGES: 277-284
- (G) DATE: 1985
- (K) RELEVANT RESIDUES IN SEQ ID NO: 37: FROM 1 TO 1040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TGTACTGTCC ATTTATCAGG ATGGAGTTCA TAACCCATCC AAAGGAATGG AGGTTCTTTC 60
TGATGTTTTT TGTCTGGTGT GGTAAAGTCCC CACCTCAACA GATGTTGTCT CAGCTCCTCT 120
ATTTTTGTTC TATGCTGCCC TATTTCTAAG TCAGATCCTA CATACAAATC ATCCATGTAT 180
TGATAGATAA CTATGTCTGG ATTTTGTTTT TTAAAAGGCT CTAAGATTTT TGTCATGCTA 240
CTTTGGAATA TTGCTGGTGA TCCTTTCCAT CCCTGTGGAA GCACATTGTA CTGATATCTA 300
ATCCCTGGTG TCTCATTGTT TATACTAGGT ATGGTAAATG CAGTATACTT CCTGAAGTCT 360
TCATCTAAGG GAACTGAAAA ATATGCATCA CCCACATCCA GTACTGTTAC TGATTTTTTC 420
TTTTTTAACC CTGCGGGATG TGGTATTCCT AATTGAACTT CCCAGAAGTC TTGAGTTCTC 480
TTATTAAGTT CTCTGAAATC TACTAATTTT CTCCATTTAG TACTGTCTTT TTTCTTTATG 540
GCAAATACTG GAGTATTGTA TGGATTCTCA GGCCCAATTT TTGAAATTTT CCCTTCCTTT 600
TCCATTTCTG TACAAATTTT TACTAATGCT TTTATTTTTT CTTCTGTCAA TGGCCATTGT 660
TTAACTTTTG GGCCATCCAT TCCTGGCTTT AATTTTACTG GTACAGTCTC AATAGGGCTA 720
ATGGGAAAT TTAAAGTGCA ACCAATCTGA GTCAACAGAT TTCTTCCAAT TATGTTGACA 780
GGTGTAGGTC CTACTAATAC TGTACCTATA GCTTTATGTC CACAGATTTT TATGAGTATC 840
TGATCATACT GTCTTACTTT GATAAAACCT CCAATTCCCC CTATCATTTT TGGTTTCCAT 900
CTTCCTGGCA AACTCATTTT TTCTAATACT GTATCATCTG CTCCTGTATC TAATAGAGCT 960
TCCTTTAGTT GCCCCCTAT CTTTATTGTG ACGAGGGGTC GTTGCCAAAG AGTGATCTGA 1020
GGGAAGTTAA AGGATACAGT 1040

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..982
- (C) IDENTIFICATION METHOD: experimental

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(ix) FEATURE:
      (A) NAME/KEY: promoter
      (B) LOCATION: 983..999
      (D) OTHER INFORMATION: /function= "promoter for T7 RNA
polymerase"
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```
(x) PUBLICATION INFORMATION:
      (A) AUTHORS: Arcari, P.
                  Martinelli, R.
                  Salvatore, F.
      (B) TITLE: The complete sequence of a full length cDNA
                  for human liver glyceraldehyde-3-phosphate
                  dehydrogenase: evidence for multiple mRNA species
      (C) JOURNAL: Nucleic Acids Res.
      (D) VOLUME: 12
      (E) ISSUE: 23
      (F) PAGES: 9179-9189
      (G) DATE: 1984
      (K) RELEVANT RESIDUES IN SEQ ID NO: 38: FROM 1 TO 999
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G	AAG	GTC	GGA	GTC	AAC	GGA	TTT	GGT	CGT	ATT	GGG	CGC	CTG	GTC	ACC	46
Lys	Val	Gly	Val	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu	Val	Thr		
1				5					10					15		
AGG	GCT	GCT	TTT	AAC	TCT	GGT	AAA	GTG	GAT	ATT	GTT	GCC	ATC	AAT	GAC	94
Arg	Ala	Ala	Phe	Asn	Ser	Gly	Lys	Val	Asp	Ile	Val	Ala	Ile	Asn	Asp	
				20					25					30		
CCC	TTC	ATT	GAC	CTC	AAC	TAC	ATG	GTT	TAC	ATG	TTC	CAA	TAT	GAT	TCC	142
Pro	Phe	Ile	Asp	Leu	Asn	Tyr	Met	Val	Tyr	Met	Phe	Gln	Tyr	Asp	Ser	
			35					40					45			
ACC	CAT	GGC	AAA	TTC	CAT	GGC	ACC	GTC	AAG	GCT	GAG	AAC	GGG	AAG	CTT	190
Thr	His	Gly	Lys	Phe	His	Gly	Thr	Val	Lys	Ala	Glu	Asn	Gly	Lys	Leu	
		50					55					60				
GTC	ATC	AAT	GGA	AAT	CCC	ATC	ACC	ATC	TTC	CAG	GAG	CGA	GAT	CCC	TCC	238
Val	Ile	Asn	Gly	Asn	Pro	Ile	Thr	Ile	Phe	Gln	Glu	Arg	Asp	Pro	Ser	
	65					70					75					
AAA	ATC	AAG	TGG	GGC	GAT	GCT	GGC	GCT	GAG	TAC	GTC	GTG	GAG	TCC	ACT	286
Lys	Ile	Lys	Trp	Gly	Asp	Ala	Gly	Ala	Glu	Tyr	Val	Val	Glu	Ser	Thr	
80					85				90					95		
GGC	GTC	TTC	ACC	ACC	ATG	GAG	AAG	GCT	GGG	GCT	CAT	TTG	CAG	GGG	GGA	334
Gly	Val	Phe	Thr	Thr	Met	Glu	Lys	Ala	Gly	Ala	His	Leu	Gln	Gly	Gly	
				100					105					110		
GCC	AAA	AGG	GTC	ATC	ATC	TCT	GCC	CCC	TCT	GCT	GAT	GCC	CCC	ATG	TTC	382

Ala	Lys	Arg	Val	Ile	Ile	Ser	Ala	Pro	Ser	Ala	Asp	Ala	Pro	Met	Phe	
			115					120					125			
GTC	ATG	GGT	GTG	AAC	CAT	GAG	AAG	TAT	GAC	AAC	AGC	CTC	AAG	ATC	ATC	430
Val	Met	Gly	Val	Asn	His	Glu	Lys	Tyr	Asp	Asn	Ser	Leu	Lys	Ile	Ile	
		130					135					140				
AGC	AAT	GCC	TCC	TGC	ACC	ACC	AAC	TGC	TTA	GCA	CCC	CTG	GCC	AAG	GTC	478
Ser	Asn	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Leu	Ala	Lys	Val	
	145						150				155					
ATC	CAT	GAC	AAC	TTT	GGT	ATC	GTG	GAA	GGA	CTC	ATG	ACC	ACA	GTC	CAT	526
Ile	His	Asp	Asn	Phe	Gly	Ile	Val	Glu	Gly	Leu	Met	Thr	Thr	Val	His	
160					165					170					175	
GCC	ATC	ACT	GCC	ACC	CAG	AAG	ACT	GTG	GAT	GGC	CCC	TCC	GGG	AAA	CTG	574
Ala	Ile	Thr	Ala	Thr	Gln	Lys	Thr	Val	Asp	Gly	Pro	Ser	Gly	Lys	Leu	
				180					185						190	
TGG	CGT	GAT	GGC	CGC	GGG	GCT	CTC	CAG	AAC	ATC	ATC	CCT	GCC	TCT	ACT	622
Trp	Arg	Asp	Gly	Arg	Gly	Ala	Leu	Gln	Asn	Ile	Ile	Pro	Ala	Ser	Thr	
			195					200					205			
GGC	GCT	GCC	AAG	GCT	GTG	GGC	AAG	GTC	ATC	CCT	GAG	CTA	GAC	GGG	AAG	670
Gly	Ala	Ala	Lys	Ala	Val	Gly	Lys	Val	Ile	Pro	Glu	Leu	Asp	Gly	Lys	
		210					215					220				
CTC	ACT	GGC	ATG	GCC	TTC	CGT	GTC	CCC	ACT	GCC	AAC	GTG	TCA	GTG	GTG	718
Leu	Thr	Gly	Met	Ala	Phe	Arg	Val	Pro	Thr	Ala	Asn	Val	Ser	Val	Val	
		225					230				235					
GAC	CTG	ACC	TGC	CGT	CTA	GAA	AAA	CCT	GCC	AAA	TAT	GAT	GAC	ATC	AAG	766
Asp	Leu	Thr	Cys	Arg	Leu	Glu	Lys	Pro	Ala	Lys	Tyr	Asp	Asp	Ile	Lys	
		240				245				250					255	
AAG	GTG	GTG	AAG	CAG	GCG	TCG	GAG	GGC	CCC	CTC	AAA	GGC	ATC	CTG	GGC	814
Lys	Val	Val	Lys	Gln	Ala	Ser	Glu	Gly	Pro	Leu	Lys	Gly	Ile	Leu	Gly	
				260					265					270		
TAC	ACT	GAG	CAC	CAG	GTG	GTC	TCC	TCT	GAC	TTC	AAC	AGC	GAC	ACC	CAC	862
Tyr	Thr	Glu	His	Gln	Val	Val	Ser	Ser	Asp	Phe	Asn	Ser	Asp	Thr	His	
			275					280					285			
TCC	TCC	ACC	TTT	GAC	GCT	GGG	GCT	GGC	ATT	GCC	CTC	AAC	GAC	CAC	TTT	910
Ser	Ser	Thr	Phe	Asp	Ala	Gly	Ala	Gly	Ile	Ala	Leu	Asn	Asp	His	Phe	
		290					295					300				
GTC	AAG	CTC	ATT	TCC	TGG	TAT	GAC	AAC	GAA	TTT	GGC	TAC	AGC	AAC	AGG	958
Val	Lys	Leu	Ile	Ser	Trp	Tyr	Asp	Asn	Glu	Phe	Gly	Tyr	Ser	Asn	Arg	
		305				310					315					
GTG	GTG	GAC	CTC	ATG	GCC	CAC	ATG	CTATAGTGAG	TCGTATT							999
Val	Val	Asp	Leu	Met	Ala	His	Met									
		320				325										

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1049 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..372
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION: /partial

/codon_start= 1
/function= "tumor suppressor"
/product= "p53 (C-terminal portion)"
/evidence= EXPERIMENTAL
/gene= "HSP53G"
/standard_name= "p53"

(ix) FEATURE:
(A) NAME/KEY: 3'UTR
(B) LOCATION: 373..1049
(D) OTHER INFORMATION: /citation= ([1])

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Futreal, P. A.
Barrett, J. C.
Wiseman, R. W.
(B) TITLE: An Alu polymorphism intragenic to the TP53
gene
(C) JOURNAL: Nucleic Acids Res.
(D) VOLUME: 19
(E) ISSUE: 24
(F) PAGES: 6977-
(G) DATE: 1991
(K) RELEVANT RESIDUES IN SEQ ID NO: 39: FROM 1 TO 1049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAG GTG CGT GTT TGT GCC TGT CCT GGG AGA GAC CGG CGC ACA GAG GAA	48
Glu Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu	
1 5 10 15	
GAG AAT CTC CGC AAG AAA GGG GAG CCT CAC CAC GAG CTG CCC CCA GGG	96
Glu Asn Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly	
20 25 30	
AGC ACT AAG CGA GCA CTG CCC AAC AAC ACC AGC TCC TCT CCC CAG CCA	144
Ser Thr Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Pro Gln Pro	
35 40 45	
AAG AAG AAA CCA CTG GAT GGA GAA TAT TTC ACC CTT CAG ATC CGT GGG	192
Lys Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly	
50 55 60	

CGT GAG CGC TTC GAG ATG TTC CGA GAG CTG AAT GAG GCC TTG GAA CTC	240
Arg Glu Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu	
65 70 75 80	
AAG GAT GCC CAG GCT GGG AAG GAG CCA GGG GGG AGC AGG GCT CAC TCC	288
Lys Asp Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser	
85 90 95	
AGC CAC CTG AAG TCC AAA AAG GGT CAG TCT ACC TCC CGC CAT AAA AAA	336
Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys	
100 105 110	
CTC ATG TTC AAG ACA GAA GGG CCT GAC TCA GAC TGA CATTCTCCAC	382
Leu Met Phe Lys Thr Glu Gly Pro Asp Ser Asp *	
115 120	
TTCTTGTTCC CCACTGACAG CCTCCCTCCC CCATCTCTCC CTCCCCTGCC ATTTTGGGTT	442
TTGGGTCTTT GAACCCTTGC TTGCAATAGG TGTGCGTCAG AAGCACCCAG GACTTCCATT	502
TGCTTTGTCC CGGGGCTCCA CTGAACAAGT TGGCCTGCAC TGGTGTTTTG TTGTGGGGAG	562
GAGGATGGGG AGTAGGACAT ACCAGCTTAG ATTTAAGGT TTTTACTGTG AGGGATGTTT	622
GGGAGATGTA AGAAATGTTT TTGCAGTTAA GGGTTAGTTT ACAATCAGCC ACATTCTAGG	682
TAGGTAGGGG CCCACTTCAC CGTACTAACC AGGGAAGCTG TCCCTCATGT TGAATTTTCT	742
CTAACTTCAA GGCCCATATC TGTGAAATGC TGGCATTTCG ACCTACCTCA CAGAGTGCAT	802
TGTGAGGGTT AATGAAATAA TGTACATCTG GCCTTGAAAC CACCTTTTAT TACATGGGGT	862
CTAAACTTG ACCCCCTTGA GGGTGCCTGT TCCCTCTCCC TCTCCCTGTT GGCTGGTGGG	922
TTGGTAGTTT CTACAGTTGG GCAGCTGGTT AGGTAGAGGG AGTTGTCAAG TCTTGCTGGC	982
CCAGCCAAAC CCTGTCTGAC AACCTCTTGG TCGACCTTAG TACCTAAAAG GAAATCTCAC	1042
CCCATCC	1049

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTCTTCCACA TTCACCT

17

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCTTCCACAT TCACCTT

17

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTCCACATT CACCTTG

17

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTCCACATTG ACCTTG

17

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCACATTCA CCTTGCC

17

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCACATTGAC CTTGCCC

17

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CACATTCACC TTGCCCC

17

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACATTCACCT TGCCCCA

17

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATTCACCTT GCCCCAC

17

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATTCACCTTG CCCCACA

17

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTCACCTTGC CCCACAG

17

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCACCTTGCC CCACAGG

17

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CACCTTGCCC CACAGGG

17

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACCTTGCCCC ACAGGGC

17

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTTGCCCCA CAGGGCA

17

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTTGCCCCAC AGGGCAG

17

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTGCCCCACA GGGCAGT

17

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGCCCCACAG GGCAGTG

17

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCCCCACAGG GCAGTGA

17

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCCCACAGGG CAGTGAC

17

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCCACAGGGC AGTGACC

17

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCACAGGGCA GTGACCG

17

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CACAGGGCAG TGACCGC

17

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAGGGCAGT GACCGCA

17

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAGGGCAGTG ACCGCAG

17

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AGGGCAGTGA CCGCAGA

17

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGGCAGTGAC CGCAGAC

17

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGCAGTGACC GCAGACT

17

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCAGTGACCG CAGACTT

17

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09714674-02504
FOOTED 4/29/2009

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGTGACCGC AGACTTC

17

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AGTGACCGCA GACTTCT

17

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTGACCGCAG ACTTCTC

17

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGACCGCAGA CTTCTCC

17

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GACCGCAGAC TTCTCCT

17

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACCGCAGACT TCTCCTC

17

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs

0971464-021504

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCGCAGACTT CTCCTCA

17

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CGCAGACTTC TCCTCAC

17

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GCAGACTTCT CCTCACT

17

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGACTTCTC CTCACTG

17

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGACTTCTCC TCACTGG

17

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GACTTCTCCT CACTGGA

17

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ACTTCTCCTC ACTGGAC

17

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTTCTCCTCA CTGGACA

17

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTCTCCTCAC TGGACAG

17

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCTCCTCACT GGACAGA

17

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTCCTCACTG GACAGAT

17

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TCCTCACTGG ACAGATG

17

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCTCACTGGA CAGATGC

17

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTCACTGGAC AGATGCA

17

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCACTGGACA GATGCAC

17

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CACTGGACAG ATGCACC

17

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ACTGGACAGA TGCACCA

17

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACAGAT GCACCAT

17

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGGACAGATG CACCATT

17

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGACAGATGC ACCATTG

17

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GACAGATGCA CCATTCT

17

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ACAGATGCAC CATTCTG

17

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CAGATGCACC ATTCTGT

17

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGATGCACCA TTCTGTC

17

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATGCACCAT TCTGTCT

17

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGCACCATT CTGTCTG

17

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGCACCATTC TGTCTGT

17

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GCACCATTCT GTCTGTT

17

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CACCATTCTG TCTGTTT

17

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ACCATTCTGT CTGTTTT

17

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CCATTCTGTC TGTTTTG

17

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATTCTGTCT GTTTGG

17

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATTCTGTCTG TTTTGGG

17

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TTCTGTCTGT TTTGGGG

17

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCTGTCTGTT TTGGGGG

17

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTGTCTGTTT TGGGGGA

17

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TGTCTGTTTT GGGGGAT

17

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GTCTGTTTTG GGGGATT

17

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCTGTTTTGG GGGATTG

17

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CTGTTTTGGG GGATTGC

17

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs

0971464-0250

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTTGGGG GATTGCA

17

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GTTTTGGGGG ATTGCAA

17

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

TTTTGGGGGA TTGCAAG

17

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTTGGGGGAT TGCAAGT

17

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TTGGGGGATT GCAAGTA

17

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

0971464-03450

TGGGGGATTG CAAGTAA

17

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGGGGATTGC AAGTAAA

17

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GGGGATTGCA AGTAAAC

17

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09784674-024501
T05T20-42948760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGGATTGCAA GTAAACA

17

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GGATTGCAAG TAAACAC

17

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GATTGCAAGT AAACACA

17

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATTGCAAGTA AACACAG

17

(2) INFORMATION FOR SEQ ID NO: 127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TTGCAAGTAA ACACAGT

17

(2) INFORMATION FOR SEQ ID NO: 128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

TGCAAGTAAA CACAGTT

17

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCAAGTAAAC ACAGTTG

17

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CAAGTAAACA CAGTTGT

17

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

AAGTAAACAC AGTTGTG

17

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10971464-024504

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

AGTAAACACA GTTGTGT

17

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GTAAACACAG TTGTGTC

17

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TAAACACAGT TGTGTCA

17

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs

10971464-021304

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

AAACACAGTT GTGTCAA

17

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

AACACAGTTG TGTCAA

17

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACACAGTTGT GTCAAAA

17

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CACAGTTGTG TCAAAAG

17

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ACAGTTGTGT CAAAAGC

17

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

10971464-021501

CAGTTGTGTC AAAAGCA

17

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AGTTGTGTCA AAAGCAA

17

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GTTGTGTCAA AAGCAAG

17

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TTGTGTCAAA AGCAAGT

17

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGTGTCAAAA GCAAGTG

17

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTACTGTCCA TTTATCAGGA

20

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TACTGTCCAT TTATCAGGAT

20

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACTGTCCATT TATCAGGATG

20

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

CTGTCCATTT ATCAGGATGG

20

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TGTCCATTTA TCAGGATGGA

20

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTCCATTTAT CAGGATGGAG

20

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TCCATTTATC AGGATGGAGT

20

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

09784674-021501

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CCATTATCA GGATGGAGTT

20

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CATTATCAG GATGGAGTTC

20

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATTATCAGG ATGGAGTTCA

20

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TTTATCAGGA TGGAGTTCAT

20

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

TTATCAGGAT GGAGTTCATA

20

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TATCAGGATG GAGTTCATAA

20

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ATCAGGATGG AGTTCATAAC

20

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TCAGGATGGA GTTCATAACC

20

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CAGGATGGAG TTCATAACCC

20

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

AGGATGGAGT TCATAACCCA

20

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GGATGGAGTT CATAACCCAT

20

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATGGAGTTC ATAACCCATC

20

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

ATGGAGTTCA TAACCCATCC

20

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TGGAGTTCAT AACCCATCCC

20

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GGAGTTCATA ACCCATCCCA

20

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAGTTCATAA CCCATCCCAA

20

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

AGTTCATAAC CCATCCCAAA

20

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GTTTCATAACC CATCCCAAAG

20

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TTCATAACCC ATCCCAAAGG

20

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TCATAACCCA TCCCAAAGGA

20

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10971464-1

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CATAACCCAT CCCAAAGGAA

20

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ATAACCCATC CCAAAGGAAT

20

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TAACCCATCC CAAAGGAATG

20

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AACCCATCCC AAAGGAATGG

20

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

ACCCATCCCA AAGGAATGGA

20

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CCCATCCCAA AGGAATGGAG

20

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CCATCCCAAA GGAATGGAGG

20

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CATCCCAAAG GAATGGAGGT

20

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ATCCCAAAGG AATGGAGGTT

20

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCCAAAGGA ATGGAGGTTT

20

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CCCAAAGGAA TGGAGGTTCT

20

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CCAAAGGAAT GGAGGTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CAAAGGAATG GAGGTTCTTT

20

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

AAAGGAATGG AGGTTCTTTC

20

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

AAGGAATGGA GGTTCCTTCT

20

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AGGAATGGAG GTTCTTTCTG

20

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GGAATGGAGG TTCTTTCTGA

20

(2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAATGGAGGT TCTTTCTGAT

20

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

AATGGAGGTT CTTTCTGATG

20

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

ATGGAGGTTC TTTCTGATGT

20

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

TGGAGGTTCT TTCTGATGTT

20

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GGAGGTTCTT TCTGATGTTT

20

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAGGTTCTTT CTGATGTTTT

20

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

AGGTTCTTTC TGATGTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTCTTTCT GATGTTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GTTCTTTCTG ATGTTTTTTG

20

(2) INFORMATION FOR SEQ ID NO: 198:

10971464-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTCTTTCTGA TGTTTTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TCTTTCTGAT GTTTTTTGTC

20

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CTTTCTGATG TTTTTTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTCTGATGT TTTTGTCTG

20

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTCTGATGTT TTTTGTCTGG

20

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

0971464-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TCTGATGTTT TTTGTCTGGT

20

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

CTGATGTTTT TTGTCTGGTG

20

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TGATGTTTTT TGTCTGGTGT

20

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GATGTTTTTT GTCTGGTGTG

20

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGTTTTTTT TCTGGTGTGG

20

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TGTTTTTTTGT CTGGTGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GTTTTTTGTC TGGTGTGGTA

20

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

TTTTTTGTCT GGTGTGGTAA

20

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TTTTTTGTCTG GTGTGGTAAG

20

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TTTTGTCTGG TGTGGTAAGT

20

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TTTGTCTGGT GTGGTAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TTGTCTGGTG TGGTAAGTCC

20

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TGTCTGGTGT GGTAAGTCCC

20

(2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GTCTGGTGTG GTAAGTCCCC

20

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

TCTGGTGTGG TAAGTCCCCA

20

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTGGTGTGGT AAGTCCCCAC

20

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TGGTGTGGTA AGTCCCCACC

20

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

0971464-1.DOC

GGTGTGGTAA GTCCCCACCT

20

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GTGTGGTAAG TCCCCACCTC

20

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGTGGTAAGT CCCCACCTCA

20

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GTGGTAAGTC CCCACCTCAA

20

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TGGTAAGTCC CCACCTCAAC

20

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGTAAGTCCC CACCTCAACA

20

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GTAAGTCCCC ACCTCAACAG

20

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

TAAGTCCCCA CCTCAACAGA

20

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

AAGTCCCCAC CTCAACAGAT

20

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

AGTCCCCACC TCAACAGATG

20

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GTCCCCACCT CAACAGATGT

20

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TCCCCACCTC AACAGATGTT

20

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

CCCCACCTCA ACAGATGTTG

20

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CCCACCTCAA CAGATGTTGT

20

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CCACCTCAAC AGATGTTGTC

20

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CACCTCAACA GATGTTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

ACCTCAACAG ATGTTGTCTC

20

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CCTCAACAGA TGTTGTCTCA

20

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCAACAGAT GTTGTCTCAG

20

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAACAGATG TTGTCTCAGC

20

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

CAACAGATGT TGTCTCAGCT

20

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

AACAGATGTT GTCTCAGCTC

20

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

ACAGATGTTG TCTCAGCTCC

20

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

03794674-021504
FOSTER 4/24/02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CAGATGTTGT CTCAGCTCCT

20

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

AGATGTTGTC TCAGCTCCTC

20

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GATGTTGTCT CAGCTCCTCT

20

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

ATGTTGTCTC AGCTCCTCTA

20

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TGTTGTCTCA GCTCCTCTAT

20

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GTTGTCTCAG CTCCTCTATT

20

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTGTCTCAGC TCCTCTATTT

20

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TGTCTCAGCT CCTCTATTTT

20

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GTCTCAGCTC CTCTATTTTT

20

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

09724674.021501

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TCTCAGCTCC TCTATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

CTCAGCTCCT CTATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TCAGCTCCTC TATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

CAGCTCCTCT ATTTTGTTC

20

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

AGCTCCTCTA TTTTGTTC

20

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GCTCCTCTAT TTTTGTTC

20

(2) INFORMATION FOR SEQ ID NO: 258:

0971464-021501

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CTCCTCTATT TTTGTTCTAT

20

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

TCCTCTATTT TTGTTCTATG

20

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

CCTCTATTTT TGTTCTATGC

20

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

CTCTATTTT GTTCTATGCT

20

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TCTATTTTGT TTCTATGCTG

20

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

0971464-1034504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

CTATTTTGT TCTATGCTGC

20

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

TATTTTGT CTATGCTGCC

20

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ATTTTGTTC TATGCTGCCC

20

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

0971464-1 021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

TTTTTGTCT ATGCTGCCCT

20

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TTTTGTCTA TGCTGCCCTA

20

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

TTTGTCTAT GCTGCCCTAT

20

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

TTGTTCTATG CTGCCCTATT

20

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

TGTTCTATGC TGCCCTATTT

20

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GTTCTATGCT GCCCTATTC

20

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

05784674.021501

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TTCTATGCTG CCCTATTTCT

20

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TCTATGCTGC CCTATTTCTA

20

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTATGCTGCC CTATTTCTAA

20

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

09784674.021501

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TATGCTGCCC TATTTCTAAG

20

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

ATGCTGCCCT ATTTCTAAGT

20

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TGCTGCCCTA TTTCTAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GCTGCCCTAT TTCTAAGTCA

20

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

CTGCCCTATT TCTAAGTCAG

20

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

TGCCCTATTT CTAAGTCAGA

20

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GCCCTATTTT TAAGTCAGAT

20

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

CCCTATTTCT AAGTCAGATC

20

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

0971464-1021504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

CCTATTTCTA AGTCAGATCC

20

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

CTATTTCTAA GTCAGATCCT

20

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

TATTTCTAAG TCAGATCCTA

20

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

ATTCTAAGT CAGATCCTAC

20

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TTTCTAAGTC AGATCCTACA

20

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

TTCTAAGTCA GATCCTACAT

20

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: NO

TCTAAGTCAG ATCCTACATA

20

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

CTAAGTCAGA TCCTACATAC

20

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TAAGTCAGAT CCTACATACA

20

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

AAGTCAGATC CTACATACAA

20

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

AGTCAGATCC TACATACAAA

20

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GTCAGATCCT ACATACAAAT

20

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

TCAGATCCTA CATACAAATC

20

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CAGATCCTAC ATACAAATCA

20

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

AGATCCTACA TACAAATCAT

20

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GATCCTACAT ACAAATCATC

20

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

ATCCTACATA CAAATCATCC

20

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

10971464-031501

TCCTACATAC AAATCATCCA

20

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

CCTACATACA AATCATCCAT

20

(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

CTACATACAA ATCATCCATG

20

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

TACATACAAA TCATCCATGT

20

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

ACATACAAAT CATCCATGTA

20

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

CATACAAATC ATCCATGTAT

20

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

ATACAAATCA TCCATGTATT

20

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

TACAAATCAT CCATGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

ACAAATCATC CATGTATTGA

20

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

CAAATCATCC ATGTATTGAT

20

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AAATCATCCA TGTATTGATA

20

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATCATCCAT GTATTGATAG

20

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

ATCATCCATG TATTGATAGA

20

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

TCATCCATGT ATTGATAGAT

20

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

CATCCATGTA TTGATAGATA

20

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

ATCCATGTAT TGATAGATAA

20

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

TCCATGTATT GATAGATAAC

20

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

CCATGTATTG ATAGATAACT

20

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

CATGTATTGA TAGATAACTA

20

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

ATGTATTGAT AGATAACTAT

20

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

TGTATTGATA GATAACTATG

20

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GTATTGATAG ATAACATATGT

20

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

TATTGATAGA TAACTATGTC

20

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ATTGATAGAT AACTATGTCT

20

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

TTGATAGATA ACTATGTCTG

20

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

TGATAGATAA CTATGTCTGG

20

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GATAGATAAC TATGTCTGGA

20

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

ATAGATAACT ATGTCTGGAT

20

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

TAGATAACTA TGTCTGGATT

20

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

AGATAACTAT GTCTGGATTT

20

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GATAACTATG TCTGGATTTT

20

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

ATAACTATGT CTGGATTTTG

20

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

TAACTATGTC TGGATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

AACTATGTCT GGATTTTGGT

20

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

ACTATGTCTG GATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

CTATGTCTGG ATTTTGTTTT

20

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

TATGTCTGGA TTTTGTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

ATGTCTGGAT TTTGTTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

TGTCTGGATT TTGTTTTTTA

20

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GTCTGGATTT TGTTTTTTAA

20

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

TCTGGATTTT GTTTTTTAAA

20

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

CTGGATTTTG TTTTTTAAAA

20

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TGGATTTTGT TTTTAAAAAG

20

(2) INFORMATION FOR SEQ ID NO: 343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GGATTTTGT TTTTAAAGG

20

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GATTTTGT TTTTAAAGGC

20

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ATTTTGT TTTTAAAGGCT

20

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

TTTGTGTTTTT TAAAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

TTTGTGTTTTT AAAAGGCTCT

20

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

TTGTTTTTTTA AAAGGCTCTA

20

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

TGTTTTTTTAA AAGGCTCTAA

20

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GTTTTTTTAAA AGGCTCTAAG

20

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

TTTTTTTAAAA GGCTCTAAGA

20

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

TTTTTAAAAG GCTCTAAGAT

20

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

TTTTAAAAGG CTCTAAGATT

20

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

TTTAAAAGGC TCTAAGATTT

20

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

TTAAAAGGCT CTAAGATTTT

20

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

TAAAAGGCTC TAAGATTTTT

20

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

AAAAGGCTCT AAGATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

AAAGGCTCTA AGATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

AAGGCTCTAA GATTTTGTGTC

20

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

AGGCTCTAAG ATTTTGTCA

20

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

GGCTCTAAGA TTTTGTGTCAT

20

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GCTCTAAGAT TTTTGTGTCATG

20

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

CTCTAAGATT TTTGTCATGC

20

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

TCTAAGATTT TTGTCATGCT

20

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

CTAAGATTTT TGTCATGCTA

20

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

TAAGATTTTT GTCATGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

AAGATTTTTG TCATGCTACT

20

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

AGATTTTTGT CATGCTACTT

20

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GATTTTGTGC ATGCTACTTT

20

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

ATTTTGTCA TGCTACTTTG

20

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

TTTTTGT CAT GCTACTTTGG

20

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10971464-1

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

TTTGTGCATG CTACTTTGGA

20

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

TTTGTGCATGC TACTTTGGAA

20

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

TTGTCATGCT ACTTTGGAAT

20

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

TGTCATGCTA CTTTGAATA

20

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GTCATGCTAC TTTGGAATAT

20

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

TCATGCTACT TTGGAATATT

20

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

CATGCTACTT TGGAATATTG

20

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ATGCTACTTT GGAATATTGC

20

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

097464-1097464-1

TGCTACTTTG GAATATTGCT

20

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GCTACTTTGG AATATTGCTG

20

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

CTACTTTGGA ATATTGCTGG

20

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(iv) ANTI-SENSE: NO

20

(iv) ANTI-SENSE: NO

20

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

TTTGAATAT TGCTGGTGAT

20

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

TTGGAATATT GCTGGTGATC

20

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TGGAATATTG CTGGTGATCC

20

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GGAATATTGC TGGTGATCCT

20

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATATTGCT GGTGATCCTT

20

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

AATATTGCTG GTGATCCTTT

20

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

ATATTGCTGG TGATCCTTTC

20

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

TATTGCTGGT GATCCTTTCC

20

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

ATTGCTGGTG ATCCTTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

09714674-021501

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

TTGCTGGTGA TCCTTTCCAT

20

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

TGCTGGTGAT CCTTTCCATC

20

(2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GCTGGTGATC CTTTCCATCC

20

(2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

CTGGTGATCC TTCCATCCC

20

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

TGGTGATCCT TTCCATCCCT

20

(2) INFORMATION FOR SEQ ID NO: 400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

09784674-021501

GGTGATCCTT TCCATCCCTG

20

(2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GTGATCCTTT CCATCCCTGT

20

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

TGATCCTTTC CATCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GATCCTTTCC ATCCCTGTGG

20

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

ATCCTTTCCA TCCCTGTGGA

20

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

TCCTTTCCAT CCCTGTGGAA

20

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

CCTTTCCATC CCTGTGGAAG

20

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

CTTTCCATCC CTGTGGAAGC

20

(2) INFORMATION FOR SEQ ID NO: 408:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

TTTCCATCCC TGTGGAAGCA

20

(2) INFORMATION FOR SEQ ID NO: 409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

TTCCATCCCT GTGGAAGCAC

20

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

TCCATCCCTG TGGAAGCACA

20

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

CCATCCCTGT GGAAGCACAT

20

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

005720 42948260

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

CATCCCTGTG GAAGCACATT

20

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

ATCCCTGTGG AAGCACATTG

20

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

TCCCTGTGGA AGCACATTGT

20

(2) INFORMATION FOR SEQ ID NO: 415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

CCCTGTGGAA GCACATTGTA

20

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

CCTGTGGAAG CACATTGTAC

20

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

CTGTGGAAGC ACATTGTACT

20

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

TGTGGAAGCA CATTGTACTG

20

(2) INFORMATION FOR SEQ ID NO: 419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GTGGAAGCAC ATTGTACTGA

20

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

TGGAAGCACA TTGTACTGAT

20

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GGAAGCACAT TGTACTGATA

20

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAAGCACATT GTACTGATAT

20

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

AAGCACATTG TACTGATATC

20

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

AGCACATTGT ACTGATATCT

20

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GCACATTGTA CTGATATCTA

20

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

CACATTGTAC TGATATCTAA

20

(2) INFORMATION FOR SEQ ID NO: 427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

ACATTGTACT GATATCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

CATTGTACTG ATATCTAATC

20

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

ATTGTACTGA TATCTAATCC

20

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

TTGTACTGAT ATCTAATCCC

20

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

TGTACTGATA TCTAATCCCT

20

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GTACTGATAT CTAATCCCTG

20

(2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

TACTGATATC TAATCCCTGG

20

(2) INFORMATION FOR SEQ ID NO: 434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

ACTGATATCT AATCCCTGGT

20

(2) INFORMATION FOR SEQ ID NO: 435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

CTGATATCTA ATCCCTGGTG

20

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

TGATATCTAA TCCCTGGTGT

20

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

GATATCTAAT CCCTGGTGTC

20

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

ATATCTAATC CCTGGTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

TATCTAATCC CTGGTGTCTC

20

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

ATCTAATCCC TGGTGTCTCA

20

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

TCTAATCCCT GGTGTCTCAT

20

(2) INFORMATION FOR SEQ ID NO: 442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

CTAATCCCTG GTGTCTCATT

20

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

TAATCCCTGG TGTCTCATTG

20

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

AATCCCTGGT GTCTCATTGT

20

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

ATCCCTGGTG TCTCATTGTT

20

(2) INFORMATION FOR SEQ ID NO: 446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

TCCCTGGTGT CTCATTGTTT

20

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

CCCTGGTGTC TCATTGTTTA

20

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

CCTGGTGTCT CATTGTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CTGGTGTCTC ATTGTTTATA

20

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

TGGTGTCTCA TTGTTTATAC

20

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GGTGTCTCAT TGTTTATACT

20

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GTGTCTCATT GTTTATACTA

20

(2) INFORMATION FOR SEQ ID NO: 453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

TGTCTCATTG TTTATACTAG

20

(2) INFORMATION FOR SEQ ID NO: 454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GTCTCATTGT TTATACTAGG

20

(2) INFORMATION FOR SEQ ID NO: 455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

TCTCATTGTT TATACTAGGT

20

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

CTCATTGTTT ATACTAGGTA

20

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

TCATTGTTTA TACTAGGTAT

20

(2) INFORMATION FOR SEQ ID NO: 458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

CATTGTTTAT ACTAGGTATG

20

(2) INFORMATION FOR SEQ ID NO: 459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

ATTGTTTATA CTAGGTATGG

20

(2) INFORMATION FOR SEQ ID NO: 460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

TTGTTTATAC TAGGTATGGT

20

(2) INFORMATION FOR SEQ ID NO: 461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

TGTTTATACT AGGTATGGTA

20

(2) INFORMATION FOR SEQ ID NO: 462:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GTTTATACTA GGTATGGTAA

20

(2) INFORMATION FOR SEQ ID NO: 463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

TTTATACTAG GTATGGTAAA

20

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

TTATACTAGG TATGGTAAAT

20

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

TATACTAGGT ATGGTAAATG

20

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

ATACTAGGTA TGGTAAATGC

20

(2) INFORMATION FOR SEQ ID NO: 467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

TACTAGGTAT GGTAATGCA

20

(2) INFORMATION FOR SEQ ID NO: 468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

ACTAGGTATG GTAAATGCAG

20

(2) INFORMATION FOR SEQ ID NO: 469:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

CTAGGTATGG TAAATGCAGT

20

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

TAGGTATGGT AAATGCAGTA

20

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

AGGTATGGTA AATGCAGTAT

20

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GGTATGGTAA ATGCAGTATA

20

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GTATGGTAAA TGCAGTATAC

20

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

TATGGTAAAT GCAGTATACT

20

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

ATGGTAAATG CAGTATACTT

20

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

TGGTAAATGC AGTATACTTC

20

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GGTAAATGCA GTATACTTCC

20

(2) INFORMATION FOR SEQ ID NO: 478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GTAAATGCAG TATACTTCCT

20

(2) INFORMATION FOR SEQ ID NO: 479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

TAAATGCAGT ATACTTCCTG

20

(2) INFORMATION FOR SEQ ID NO: 480:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

AAATGCAGTA TACTTCCTGA

20

(2) INFORMATION FOR SEQ ID NO: 481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

AATGCAGTAT ACTTCCTGAA

20

(2) INFORMATION FOR SEQ ID NO: 482:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

ATGCAGTATA CTCCTGAAG

20

(2) INFORMATION FOR SEQ ID NO: 483:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

TGCAGTATAC TTCCTGAAGT

20

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GCAGTATACT TCCTGAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

CAGTATACTT CCTGAAGTCT

20

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

AGTATACTTC CTGAAGTCTT

20

(2) INFORMATION FOR SEQ ID NO: 487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GTATACTTCC TGAAGTCTTC

20

(2) INFORMATION FOR SEQ ID NO: 488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

TATACTTCCT GAAGTCTTCA

20

(2) INFORMATION FOR SEQ ID NO: 489:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

ATACTTCCTG AAGTCTTCAT

20

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

TACTTCCTGA AGTCTTCATC

20

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

ACTTCCTGAA GTCTTCATCT

20

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CTTCCTGAAG TCTTCATCTA

20

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

TTCCTGAAGT CTTTCATCTAA

20

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

TCCTGAAGTC TTCATCTAAG

20

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

CCTGAAGTCT TCATCTAAGG

20

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

CTGAAGTCTT CATCTAAGGG

20

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

TGAAGTCTTC ATCTAAGGGA

20

(2) INFORMATION FOR SEQ ID NO: 498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

GAAGTCTTCA TCTAAGGGAA

20

(2) INFORMATION FOR SEQ ID NO: 499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

AAGTCTTCAT CTAAGGGAAC

20

(2) INFORMATION FOR SEQ ID NO: 500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

AGTCTTCATC TAAGGGAAC

20

(2) INFORMATION FOR SEQ ID NO: 501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GTCTTCATCT AAGGGAAC

20

(2) INFORMATION FOR SEQ ID NO: 502:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

TCTTCATCTA AGGGAAC

20

(2) INFORMATION FOR SEQ ID NO: 503:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

0971464-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

CTTCATCTAA GGGAAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 504:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

TTCATCTAAG GGGAAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

TCATCTAAGG GGAAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 506:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

CATCTAAGGG AACTGAAAAA

20

(2) INFORMATION FOR SEQ ID NO: 507:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

ATCTAAGGGA ACTGAAAAAT

20

(2) INFORMATION FOR SEQ ID NO: 508:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

TCTAAGGGAA CTGAAAAATA

20

(2) INFORMATION FOR SEQ ID NO: 509:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CTAAGGGAAC TGAAAAATAT

20

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

TAAGGGAAC TAAAAATATG

20

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

AAGGGAAC TG AAAAATATGC

20

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

0971464-021504

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

AGGGAAGTGA AAAATATGCA

20

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GGGAAGTGA AAATATGCAT

20

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GGAAGTGA AAATATGCATC

20

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GAACTGAAAA ATATGCATCA

20

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

AACTGAAAAA TATGCATCAC

20

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

ACTGAAAAAT ATGCATCACC

20

(2) INFORMATION FOR SEQ ID NO: 518:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

CTGAAAAATA TGCATCACCC

20

(2) INFORMATION FOR SEQ ID NO: 519:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

TGAAAAATAT GCATCACCCA

20

(2) INFORMATION FOR SEQ ID NO: 520:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GAAAAATATG CATCACCCAC

20

(2) INFORMATION FOR SEQ ID NO: 521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

AAAAATATGC ATCACCCACA

20

(2) INFORMATION FOR SEQ ID NO: 522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

AAAATATGCA TCACCCACAT

20

(2) INFORMATION FOR SEQ ID NO: 523:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

AAATATGCAT CACCCACATC

20

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

AATATGCATC ACCCACATCC

20

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

ATATGCATCA CCCACATCCA

20

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

TATGCATCAC CCACATCCAG

20

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

ATGCATCACC CACATCCAGT

20

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

TGCATCACCC ACATCCAGTA

20

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GCATCACCCA CATCCAGTAC

20

(2) INFORMATION FOR SEQ ID NO: 530:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

CATCACCCAC ATCCAGTACT

20

(2) INFORMATION FOR SEQ ID NO: 531:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

ATCACCCACA TCCAGTACTG

20

(2) INFORMATION FOR SEQ ID NO: 532:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

0971464-021501

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

TCACCCACAT CCAGTACTGT

20

(2) INFORMATION FOR SEQ ID NO: 533:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

CACCCACATC CAGTACTGTT

20

(2) INFORMATION FOR SEQ ID NO: 534:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

ACCCACATCC AGTACTGTTA

20

(2) INFORMATION FOR SEQ ID NO: 535:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

CCCACATCCA GTACTGTTAC

20

(2) INFORMATION FOR SEQ ID NO: 536:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

CCACATCCAG TACTGTTACT

20

(2) INFORMATION FOR SEQ ID NO: 537:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

CACATCCAGT ACTGTTACTG

20

(2) INFORMATION FOR SEQ ID NO: 538:

09784674-021501

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

ACATCCAGTA CTGTTACTGA

20

(2) INFORMATION FOR SEQ ID NO: 539:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

CATCCAGTAC TGTACTGAT

20

(2) INFORMATION FOR SEQ ID NO: 540:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

ATCCAGTACT GTTACTGATT

20

(2) INFORMATION FOR SEQ ID NO: 541:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

TCCAGTACTG TTACTGATTT

20

(2) INFORMATION FOR SEQ ID NO: 542:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

CCAGTACTGT TACTGATTTT

20

(2) INFORMATION FOR SEQ ID NO: 543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

CAGTACTGTT ACTGATTTTT

20

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

AGTACTGTTA CTGATTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GTACTGTTAC TGATTTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

TACTGTTACT GATTTTTTCT

20

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

ACTGTTACTG ATTTTTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

CTGTTACTGA TTTTTTCTTT

20

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

TGTTACTGAT TTTTCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 550:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GTTACTGATT TTTTCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 551:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

TTACTGATTT TTTCTTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 552:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

TACTGATTTT TTCTTTTSTA

20

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

ACTGATTTTT TCTTTTTTAA

20

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

CTGATTTTTT CTTTTTTAAC

20

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

09784674-024504

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

TGATTTTTTC TTTTAAACC

20

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GATTTTTTCT TTTTAAACC

20

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

ATTTTTTCTT TTTTAAACCCT

20

(2) INFORMATION FOR SEQ ID NO: 558:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

TTTTTTCTTT TTAAACCCTG

20

(2) INFORMATION FOR SEQ ID NO: 559:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

TTTTTCTTTT TTAACCCTGC

20

(2) INFORMATION FOR SEQ ID NO: 560:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

FOIA b 7 - EXEMPT

TTTTCTTTTT TAACCCTGCG

20

(2) INFORMATION FOR SEQ ID NO: 561:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TTTCTTTTTT AACCTGCGG

20

(2) INFORMATION FOR SEQ ID NO: 562:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

TTCTTTTTTA ACCCTGCGGG

20

(2) INFORMATION FOR SEQ ID NO: 563:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

TCTTTTTTTAA CCCTGCGGGA

20

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

CTTTTTTTAAC CCTGCGGGAT

20

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

TTTTTTTAACC CTGCGGGATG

20

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

TTTTTAACCC TCGGGGATGT

20

(2) INFORMATION FOR SEQ ID NO: 567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

TTTTAACCCCT GCGGGATGTG

20

(2) INFORMATION FOR SEQ ID NO: 568:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TTTAACCCTG CGGGATGTGG

20

(2) INFORMATION FOR SEQ ID NO: 569:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

TTAACCCTGC GGGATGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 570:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TAACCCTGCG GGATGTGGTA

20

(2) INFORMATION FOR SEQ ID NO: 571:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

AACCCTGCGG GATGTGGTAT

20

(2) INFORMATION FOR SEQ ID NO: 572:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

ACCCTGCGGG ATGTGGTATT

20

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

CCCTGCGGGA TGTGGTATTC

20

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

CCTGCGGGAT GTGGTATTCC

20

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

CTGCGGGATG TGGTATTCCT

20

(2) INFORMATION FOR SEQ ID NO: 576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

TGCGGGATGT GGTATTCCTA

20

(2) INFORMATION FOR SEQ ID NO: 577:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GCGGGATGTG GTATTCCTAA

20

(2) INFORMATION FOR SEQ ID NO: 578:

10971464-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

CGGGATGTGG TATTCCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GGGATGTGGT ATTCCTAATT

20

(2) INFORMATION FOR SEQ ID NO: 580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GGATGTGGTA TTCCTAATTG

20

(2) INFORMATION FOR SEQ ID NO: 581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GATGTGGTAT TCCTAATTGA

20

(2) INFORMATION FOR SEQ ID NO: 582:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

ATGTGGTATT CCTAATTGAA

20

(2) INFORMATION FOR SEQ ID NO: 583:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

TGTGGTATTC CTAATTGAAC

20

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GTGGTATTCC TAATTGAACT

20

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

TGGTATTCCT AATTGAACTT

20

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GGTATTCCTA ATTGAAC TTC

20

(2) INFORMATION FOR SEQ ID NO: 587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

G TATTCCTAA TTGAAC TTC

20

(2) INFORMATION FOR SEQ ID NO: 588:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

TATTCCTAAT TGAAC TTC

20

(2) INFORMATION FOR SEQ ID NO: 589:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

ATTCCTAATT GAACTTCCCA

20

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

TTCCTAATTG AACTTCCCAG

20

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

TCCTAATTGA ACTTCCCAGA

20

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

CCTAATTGAA CTTCCCAGAA

20

(2) INFORMATION FOR SEQ ID NO: 593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

CTAATTGAAC TTCCCAGAAG

20

(2) INFORMATION FOR SEQ ID NO: 594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

TAATTGAACT TCCCAGAAGT

20

(2) INFORMATION FOR SEQ ID NO: 595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

AATTGAACTT CCCAGAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

ATTGAACTTC CCAGAAGTCT

20

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

TTGAACTTCC CAGAAGTCTT

20

(2) INFORMATION FOR SEQ ID NO: 598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

TGAACTTCCC AGAAGTCTTG

20

(2) INFORMATION FOR SEQ ID NO: 599:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GAACTTCCCA GAAGTCTTGA

20

(2) INFORMATION FOR SEQ ID NO: 600:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

AACTTCCCAG AAGTCTTGAG

20

(2) INFORMATION FOR SEQ ID NO: 601:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

ACTTCCCAGA AGTCTTGAGT

20

(2) INFORMATION FOR SEQ ID NO: 602:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

CTTCCCAGAA GTCTTGAGTT

20

(2) INFORMATION FOR SEQ ID NO: 603:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

TTCCCAGAAG TCTTGAGTTC

20

(2) INFORMATION FOR SEQ ID NO: 604:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

TCCCAGAAGT CTTGAGTTCT

20

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

CCCAGAAGTC TTGAGTTCTC

20

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

CCAGAAGTCT TGAGTTCTCT

20

(2) INFORMATION FOR SEQ ID NO: 607:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

CAGAAGTCTT GAGTTCTCTT

20

(2) INFORMATION FOR SEQ ID NO: 608:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

AGAAGTCTTG AGTTCTCTTA

20

(2) INFORMATION FOR SEQ ID NO: 609:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10971464-1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GAAGTCTTGA GTTCTCTTAT

20

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

AAGTCTTGAG TTCTCTTATT

20

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

AGTCTTGAGT TCTCTTATTA

20

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GTCTTGAGTT CTCTTATTAA

20

(2) INFORMATION FOR SEQ ID NO: 613:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

TCTTGAGTTC TCTTATTAAG

20

(2) INFORMATION FOR SEQ ID NO: 614:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

CTTGAGTTCT CTTATTAAGT

20

(2) INFORMATION FOR SEQ ID NO: 615:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

TTGAGTTCTC TTATTAAGTT

20

(2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

TGAGTTCTCT TATTAAGTTC

20

(2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GAGTTCTCTT ATTAAGTTCT

20

(2) INFORMATION FOR SEQ ID NO: 618:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

AGTTCTCTTA TTAAGTTCTC

20

(2) INFORMATION FOR SEQ ID NO: 619:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GTTCTCTTAT TAAGTTCTCT

20

(2) INFORMATION FOR SEQ ID NO: 620:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

TTCTCTTATT AAGTTCTCTG

20

(2) INFORMATION FOR SEQ ID NO: 621:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

TCTCTTATTA AGTTCTCTGA

20

(2) INFORMATION FOR SEQ ID NO: 622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

CTCTTATTAA GTTCTCTGAA

20

(2) INFORMATION FOR SEQ ID NO: 623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

TCTTATTAAG TTCTCTGAAA

20

(2) INFORMATION FOR SEQ ID NO: 624:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

CTTATTAAGT TCTCTGAAAT

20

(2) INFORMATION FOR SEQ ID NO: 625:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

TTATTAAGTT CTCTGAAATC

20

(2) INFORMATION FOR SEQ ID NO: 626:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

TATTAAGTTC TCTGAAATCT

20

(2) INFORMATION FOR SEQ ID NO: 627:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

ATTAAGTTCT CTGAAATCTA

20

(2) INFORMATION FOR SEQ ID NO: 628:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

TTAAGTTCTC TGAAATCTAC

20

(2) INFORMATION FOR SEQ ID NO: 629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

TAAGTTCTCT GAAATCTACT

20

(2) INFORMATION FOR SEQ ID NO: 630:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

AAGTTCTCTG AAATCTACTA

20

(2) INFORMATION FOR SEQ ID NO: 631:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

AGTTCTCTGA AATCTACTAA

20

(2) INFORMATION FOR SEQ ID NO: 632:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

0971464-0250
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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GTTCTCTGAA ATCTACTAAT

20

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

TTCTCTGAAA TCTACTAATT

20

(2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

TCTCTGAAAT CTACTAATTT

20

(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

CTCTGAAATC TACTAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

TCTGAAATCT ACTAATTTTC

20

(2) INFORMATION FOR SEQ ID NO: 637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

CTGAAATCTA CTAATTTTCT

20

(2) INFORMATION FOR SEQ ID NO: 638:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

TGAAATCTAC TAATTTTCTC

20

(2) INFORMATION FOR SEQ ID NO: 639:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GAAATCTACT AATTTTCTCC

20

(2) INFORMATION FOR SEQ ID NO: 640:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

AAATCTACTA ATTTTCTCCA

20

(2) INFORMATION FOR SEQ ID NO: 641:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

AATCTACTAA TTTTCTCCAT

20

(2) INFORMATION FOR SEQ ID NO: 642:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

ATCTACTAAT TTTCTCCATT

20

(2) INFORMATION FOR SEQ ID NO: 643:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

TCTACTAATT TTCTCCATTT

20

(2) INFORMATION FOR SEQ ID NO: 644:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

CTACTAATTT TCTCCATTTA

20

(2) INFORMATION FOR SEQ ID NO: 645:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

TACTAATTTT CTCCATTTAG

20

(2) INFORMATION FOR SEQ ID NO: 646:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

ACTAATTTTC TCCATTTAGT

20

(2) INFORMATION FOR SEQ ID NO: 647:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

CTAATTTTCT CCATTTAGTA

20

(2) INFORMATION FOR SEQ ID NO: 648:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

TAATTTTCTC CATTTAGTAC

20

(2) INFORMATION FOR SEQ ID NO: 649:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

AATTTTCTCC ATTTAGTACT

20

(2) INFORMATION FOR SEQ ID NO: 650:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

ATTTTCTCCA TTTAGTACTG

20

(2) INFORMATION FOR SEQ ID NO: 651:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

TTTTCTCCAT TTAGTACTGT

20

(2) INFORMATION FOR SEQ ID NO: 652:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

TTTCTCCATT TAGTACTGTC

20

(2) INFORMATION FOR SEQ ID NO: 653:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

TTCTCCATTT AGTACTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 654:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

TCTCCATT TA GTACTGTCTT

20

(2) INFORMATION FOR SEQ ID NO: 655:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

CTCCATTTAG TACTGTCTTT

20

(2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

TCCATTTAGT ACTGTCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

CCATTTAGTA CTGTCTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 658:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

CATTAGTAC TGTCTTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 659:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

ATTAGTACT GTCTTTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 660:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

TTTAGTACTG TCTTTTTTCT

20

(2) INFORMATION FOR SEQ ID NO: 661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

TTAGTACTGT CTTTTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

TAGTACTGTC TTTTTTCTTT

20

(2) INFORMATION FOR SEQ ID NO: 663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

TTAGTACTGT CTTTTTCTT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

AGTACTGTCT TTTTCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 664:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GTACTGTCTT TTTTCTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

TACTGTCTTT TTTCTTTATG

20

(2) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

ACTGTCTTTT TTCTTTATGG

20

(2) INFORMATION FOR SEQ ID NO: 667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

CTGTCTTTTT TCTTTATGGC

20

(2) INFORMATION FOR SEQ ID NO: 668:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

TGTCTTTTTT CTTTATGGCA

20

(2) INFORMATION FOR SEQ ID NO: 669:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GTCTTTTTTTC TTTATGGCAA

20

(2) INFORMATION FOR SEQ ID NO: 670:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

TCTTTTTTCT TTATGGCAAA

20

(2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

CTTTTTTCTT TATGGCAAAT

20

(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

TTTTTCTTT ATGGCAAATA

20

(2) INFORMATION FOR SEQ ID NO: 673:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

TTTTTCTTTA TGGCAAATAC

20

(2) INFORMATION FOR SEQ ID NO: 674:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

TTTCTTTTAT GGCAAATACT

20

(2) INFORMATION FOR SEQ ID NO: 675:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

TTTCTTTATG GCAAATACTG

20

(2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

TTCTTTATGG CAAATACTGG

20

(2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

TCTTTATGGC AAATACTGGA

20

(2) INFORMATION FOR SEQ ID NO: 678:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

CTTTATGGCA AATACTGGAG

20

(2) INFORMATION FOR SEQ ID NO: 679:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

TTTATGGCAA ATACTGGAGT

20

(2) INFORMATION FOR SEQ ID NO: 680:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

TTATGGCAAA TACTGGAGTA

20

(2) INFORMATION FOR SEQ ID NO: 681:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

TATGGCAAAT ACTGGAGTAT

20

(2) INFORMATION FOR SEQ ID NO: 682:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

ATGGCAAATA CTGGAGTATT

20

(2) INFORMATION FOR SEQ ID NO: 683:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

TGGCAAATAC TGGAGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 684:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GGCAAATACT GGAGTATTGT

20

(2) INFORMATION FOR SEQ ID NO: 685:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GCAAATACTG GAGTATTGTA

20

(2) INFORMATION FOR SEQ ID NO: 686:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

CAAATACTGG AGTATTGTAT

20

(2) INFORMATION FOR SEQ ID NO: 687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

AAATACTGGA GTATTGTATG

20

(2) INFORMATION FOR SEQ ID NO: 688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

AATACTGGAG TATTGTATGG

20

(2) INFORMATION FOR SEQ ID NO: 689:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

ATACTGGAGT ATTGTATGGA

20

(2) INFORMATION FOR SEQ ID NO: 690:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

TACTGGAGTA TTGTATGGAT

20

(2) INFORMATION FOR SEQ ID NO: 691:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

ACTGGAGTAT TGTATGGATT

20

(2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

CTGGAGTATT GTATGGATTTC

20

(2) INFORMATION FOR SEQ ID NO: 693:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

TGGAGTATTG TATGGATTCT

20

(2) INFORMATION FOR SEQ ID NO: 694:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GGAGTATTGT ATGGATTCTC

20

(2) INFORMATION FOR SEQ ID NO: 695:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GAGTATTGTA TGGATTCTCA

20

(2) INFORMATION FOR SEQ ID NO: 696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

AGTATTGTAT GGATTCTCAG

20

(2) INFORMATION FOR SEQ ID NO: 697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GTATTGTATG GATTCTCAGG

20

(2) INFORMATION FOR SEQ ID NO: 698:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

TATTGTATGG ATTCTCAGGC

20

(2) INFORMATION FOR SEQ ID NO: 699:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

ATTGTATGGA TTCTCAGGCC

20

(2) INFORMATION FOR SEQ ID NO: 700:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

09784674-021504
T05T20-42948250

TTGTATGGAT TCTCAGGCCC

20

(2) INFORMATION FOR SEQ ID NO: 701:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

TGTATGGATT CTCAGGCCCA

20

(2) INFORMATION FOR SEQ ID NO: 702:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GTATGGATTTC TCAGGCCCAA

20

(2) INFORMATION FOR SEQ ID NO: 703:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

TTGTATGGAT TCTCAGGCCC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

TATGGATTCT CAGGCCCAAT

20

(2) INFORMATION FOR SEQ ID NO: 704:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

ATGGATTCTC AGGCCCAATT

20

(2) INFORMATION FOR SEQ ID NO: 705:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

TGGATTCTCA GGCCCAATT

20

(2) INFORMATION FOR SEQ ID NO: 706:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GGATTCTCAG GCCCAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GATTCTCAGG CCCAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 708:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

ATTCTCAGGC CCAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 709:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

TTCTCAGGCC CAATTTTGA

20

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TCTCAGGCC AATTTTGA

20

(2) INFORMATION FOR SEQ ID NO: 711:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

CTCAGGCCCA ATTTTGA

20

(2) INFORMATION FOR SEQ ID NO: 712:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

TCAGGCCCAA TTTTGAAT

20

(2) INFORMATION FOR SEQ ID NO: 713:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

CAGGCCCAAT TTTTGAAT

20

(2) INFORMATION FOR SEQ ID NO: 714:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

AGGCCCAATT TTTGAAATTT

20

(2) INFORMATION FOR SEQ ID NO: 715:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GGCCCAATTT TTGAAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

GCCCAATTTT TGAAATTTTC

20

(2) INFORMATION FOR SEQ ID NO: 717:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

CCCAATTTT GAAATTTTCC

20

(2) INFORMATION FOR SEQ ID NO: 718:

10971464-021501

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

CCAATTTTGTG AAATTTTCCC

20

(2) INFORMATION FOR SEQ ID NO: 719:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

CAATTTTGTGA AATTTTCCCT

20

(2) INFORMATION FOR SEQ ID NO: 720:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

AATTTTGTAA ATTTTCCCTT

20

(2) INFORMATION FOR SEQ ID NO: 721:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

ATTTTGTAAA TTTTCCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 722:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

TTTTTGAAAT TTTCCCTTCC

20

(2) INFORMATION FOR SEQ ID NO: 723:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

TTTTGAAATT TTCCCTTCCT

20

(2) INFORMATION FOR SEQ ID NO: 724:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

TTTGAAATTT TCCCTTCCTT

20

(2) INFORMATION FOR SEQ ID NO: 725:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

TTGAAATTTT CCCTTCCTTT

20

(2) INFORMATION FOR SEQ ID NO: 726:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

TGAAATTTTC CCTTCCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 727:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GAAATTTTCC CTTCTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 728:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

AAATTTTCCC TTCCTTTTCC

20

(2) INFORMATION FOR SEQ ID NO: 729:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

AATTTTCCCT TCCTTTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 730:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

ATTTTCCCTT CCTTTTCCAT

20

(2) INFORMATION FOR SEQ ID NO: 731:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

TTTTCCTTC CTTTTCATT

20

(2) INFORMATION FOR SEQ ID NO: 732:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10971464-1

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

TTTCCCTTCC TTTTCCATTT

20

(2) INFORMATION FOR SEQ ID NO: 733:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

TTCCCTTCCT TTTCCATTTT

20

(2) INFORMATION FOR SEQ ID NO: 734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

TCCCTTCCTT TTCCATTTCT

20

(2) INFORMATION FOR SEQ ID NO: 735:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

CCCTTCCTTT TCCATTCTG

20

(2) INFORMATION FOR SEQ ID NO: 736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

CCTTCCTTTT CCATTCTGT

20

(2) INFORMATION FOR SEQ ID NO: 737:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

CTTCCTTTTC CATTCTGTA

20

(2) INFORMATION FOR SEQ ID NO: 738:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

TTCCTTTTCC ATTTCTGTAC

20

(2) INFORMATION FOR SEQ ID NO: 739:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

TCCTTTTCCA TTTCTGTACA

20

(2) INFORMATION FOR SEQ ID NO: 740:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

CCTTTTCCAT TTCTGTACAA

20

(2) INFORMATION FOR SEQ ID NO: 741:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

CTTTTCCATT TCTGTACAAA

20

(2) INFORMATION FOR SEQ ID NO: 742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

TTTTCCATTT CTGTACAAAT

20

(2) INFORMATION FOR SEQ ID NO: 743:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

TTTCCATTTC TGTACAAATT

20

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

TTCCATTCTCT GTACAAATTT

20

(2) INFORMATION FOR SEQ ID NO: 745:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

TCCATTCTCTG TACAAATTC

20

(2) INFORMATION FOR SEQ ID NO: 746:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

CCATTTCTGT ACAAATTTCT

20

(2) INFORMATION FOR SEQ ID NO: 747:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

CATTTCTGTA CAAATTTCTA

20

(2) INFORMATION FOR SEQ ID NO: 748:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

ATTTCTGTAC AAATTTCTAC

20

(2) INFORMATION FOR SEQ ID NO: 749:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

TTTCTGTACA AATTTCTACT

20

(2) INFORMATION FOR SEQ ID NO: 750:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

TTCTGTACAA ATTTCTACTA

20

(2) INFORMATION FOR SEQ ID NO: 751:

(i) SEQUENCE CHARACTERISTICS: .
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

TCTGTACAAA TTTCTACTAA

20

(2) INFORMATION FOR SEQ ID NO: 752:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

CTGTACAAAT TTCTACTAAT

20

(2) INFORMATION FOR SEQ ID NO: 753:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

TGTACAAATT TCTACTAATG

20

(2) INFORMATION FOR SEQ ID NO: 754:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GTACAAATTT CTACTAATGC

20

(2) INFORMATION FOR SEQ ID NO: 755:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

TACAAATTTCTACTAATGCT

20

(2) INFORMATION FOR SEQ ID NO: 756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

ACAAATTTCTACTAATGCTT

20

(2) INFORMATION FOR SEQ ID NO: 757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

CAAATTTCTACTAATGCTTT

20

(2) INFORMATION FOR SEQ ID NO: 758:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

AAATTTCTAC TAATGCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 759:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

AATTTCTACT AATGCTTTTA

20

(2) INFORMATION FOR SEQ ID NO: 760:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

10971464-02450

ATTTCTACTA ATGCTTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 761:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

TTTCTACTAA TGCTTTTATT

20

(2) INFORMATION FOR SEQ ID NO: 762:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

TTCTACTAAT GCTTTTATTT

20

(2) INFORMATION FOR SEQ ID NO: 763:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

TCTACTAATG CTTTATTTT

20

(2) INFORMATION FOR SEQ ID NO: 764:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

CTACTAATGC TTTTATTTT

20

(2) INFORMATION FOR SEQ ID NO: 765:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

TACTAATGCT TTTATTTT

20

(2) INFORMATION FOR SEQ ID NO: 766:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

ACTAATGCTT TTATTTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 767:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

CTAATGCTTT TATTTTTTCT

20

(2) INFORMATION FOR SEQ ID NO: 768:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

TAATGCTTTT ATTTTTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 769:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

AATGCTTTTA TTTTCTTC

20

(2) INFORMATION FOR SEQ ID NO: 770:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

ATGCTTTTAT TTTTCTTCT

20

(2) INFORMATION FOR SEQ ID NO: 771:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

TGCTTTTATT TTTTCTTCTG

20

(2) INFORMATION FOR SEQ ID NO: 772:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GCTTTTATTT TTTCTTCTGT

20

(2) INFORMATION FOR SEQ ID NO: 773:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

CTTTTATTTT TTCTTCTGTC

20

(2) INFORMATION FOR SEQ ID NO: 774:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

TTTTATTTTT TCTTCTGTCA

20

(2) INFORMATION FOR SEQ ID NO: 775:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

TTTATTTTTTT CTTCTGTCAA

20

(2) INFORMATION FOR SEQ ID NO: 776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

TTATTTTTTTC TTCTGTCAAT

20

(2) INFORMATION FOR SEQ ID NO: 777:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

TATTTTTTCT TCTGTCAATG

20

(2) INFORMATION FOR SEQ ID NO: 778:

10971464-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

ATTTTTCTT CTGTCAATGG

20

(2) INFORMATION FOR SEQ ID NO: 779:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

TTTTTCTTC TGTCAATGGC

20

(2) INFORMATION FOR SEQ ID NO: 780:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

10971464-1

TTTTTCTTCT GTCAATGGCC

20

(2) INFORMATION FOR SEQ ID NO: 781:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

TTTTCTTCTG TCAATGGCCA

20

(2) INFORMATION FOR SEQ ID NO: 782:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

TTTCTTCTGT CAATGGCCAT

20

(2) INFORMATION FOR SEQ ID NO: 783:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

TTCTTCTGTC AATGGCCATT

20

(2) INFORMATION FOR SEQ ID NO: 784:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

TCTTCTGTCA ATGGCCATTG

20

(2) INFORMATION FOR SEQ ID NO: 785:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

CTTCTGTCAA TGGCCATTGT

20

(2) INFORMATION FOR SEQ ID NO: 786:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

TTCTGTCAAT GGCCATTGTT

20

(2) INFORMATION FOR SEQ ID NO: 787:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

TCTGTCAATG GCCATTGTTT

20

(2) INFORMATION FOR SEQ ID NO: 788:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

CTGTCAATGG CCATTGTTTA

20

(2) INFORMATION FOR SEQ ID NO: 789:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

TGTCAATGGC CATTGTTTAA

20

(2) INFORMATION FOR SEQ ID NO: 790:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GTCAATGGCC ATTGTTTAAC

20

(2) INFORMATION FOR SEQ ID NO: 791:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

TCAATGGCCA TTGTTTAACT

20

(2) INFORMATION FOR SEQ ID NO: 792:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

CAATGGCCAT TGTTTAACTT

20

(2) INFORMATION FOR SEQ ID NO: 793:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

AATGGCCATT GTTTAACTTT

20

(2) INFORMATION FOR SEQ ID NO: 794:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

ATGGCCATTG TTAACTTTT

20

(2) INFORMATION FOR SEQ ID NO: 795:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

TGGCCATTGT TTAACITTTTG

20

(2) INFORMATION FOR SEQ ID NO: 796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GGCCATTGTT TAACTTTTGG

20

(2) INFORMATION FOR SEQ ID NO: 797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GCCATTGTTT AACTTTTGGG

20

(2) INFORMATION FOR SEQ ID NO: 798:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

CCATTGTTTA ACTTTTGGGC

20

(2) INFORMATION FOR SEQ ID NO: 799:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

CATTGTTTAA CTTTGGGCC

20

(2) INFORMATION FOR SEQ ID NO: 800:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

05784674.031501
TOSTO 42948250

ATTGTTTAAC TTTGGGCCA

20

(2) INFORMATION FOR SEQ ID NO: 801:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

TTGTTTAACT TTTGGGCCAT

20

(2) INFORMATION FOR SEQ ID NO: 802:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

TGTTTAACTT TTGGGCCATC

20

(2) INFORMATION FOR SEQ ID NO: 803:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

GTTTAACTTT TGGGCCATCC

20

(2) INFORMATION FOR SEQ ID NO: 804:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

TTTAACTTTT GGGCCATCCA

20

(2) INFORMATION FOR SEQ ID NO: 805:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

TTAACTTTTG GGCCATCCAT

20

(2) INFORMATION FOR SEQ ID NO: 806:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

TAACTTTTGG GCCATCCATT

20

(2) INFORMATION FOR SEQ ID NO: 807:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

AACTTTTGGG CCATCCATTC

20

(2) INFORMATION FOR SEQ ID NO: 808:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

ACTTTTGGGC CATCCATTCC

20

(2) INFORMATION FOR SEQ ID NO: 809:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

CTTTTGGGCC ATCCATTCCT

20

(2) INFORMATION FOR SEQ ID NO: 810:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

TTTTGGGCCA TCCATTCCTG

20

(2) INFORMATION FOR SEQ ID NO: 811:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

TTTGGGCCAT CCATTCCTGG

20

(2) INFORMATION FOR SEQ ID NO: 812:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

0971464-1 021501

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

TTGGGCCATC CATTCTGGC

20

(2) INFORMATION FOR SEQ ID NO: 813:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

TGGGCCATCC ATTCCTGGCT

20

(2) INFORMATION FOR SEQ ID NO: 814:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GGGCCATCCA TTCCTGGCTT

20

(2) INFORMATION FOR SEQ ID NO: 815:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GGCCATCCAT TCCTGGCTTT

20

(2) INFORMATION FOR SEQ ID NO: 816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GCCATCCATT CCTGGCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

CCATCCATTC CTGGCTTTAA

20

(2) INFORMATION FOR SEQ ID NO: 818:

09781674-024504
T05T20-42918260

- (ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: NO

CATCCATTCC TGGCTTTAAT

(2) INFORMATION FOR SEQ ID NO: 819:

- (ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: NO

ATCCATTCCT GGCTTTAATT

(2) INFORMATION FOR SEQ ID NO: 820:

- (ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: NO

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TCCATTCCTG GCTTTAATTT

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(2) INFORMATION FOR SEQ ID NO: 821:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

CCATTCCTGG CTTTAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 822:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

CATTCCTGGC TTTAATTTTA

20

(2) INFORMATION FOR SEQ ID NO: 823:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

ATTCCTGGCT TTAATTTTAC

20

(2) INFORMATION FOR SEQ ID NO: 824:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

TTCCTGGCTT TAATTTTACT

20

(2) INFORMATION FOR SEQ ID NO: 825:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

TCCTGGCTTT AATTTTACTG

20

(2) INFORMATION FOR SEQ ID NO: 826:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

CCTGGCTTTA ATTTTACTGG

20

(2) INFORMATION FOR SEQ ID NO: 827:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

CTGGCTTTAA TTTTACTGGT

20

(2) INFORMATION FOR SEQ ID NO: 828:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

TGGCTTTAAT TTTACTGGTA

20

(2) INFORMATION FOR SEQ ID NO: 829:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GGCTTTAATT TTACTGGTAC

20

(2) INFORMATION FOR SEQ ID NO: 830:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GCTTTAATTT TACTGGTACA

20

(2) INFORMATION FOR SEQ ID NO: 831:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

CTTTAATTTT ACTGGTACAG

20

(2) INFORMATION FOR SEQ ID NO: 832:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

TTTAATTTTA CTGGTACAGT

20

(2) INFORMATION FOR SEQ ID NO: 833:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

TTAATTTTAC TGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO: 834:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

TAATTTTACT GGTACAGTCT

20

(2) INFORMATION FOR SEQ ID NO: 835:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

AATTTTACTG GTACAGTCTC

20

(2) INFORMATION FOR SEQ ID NO: 836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

ATTTTACTGG TACAGTCTCA

20

(2) INFORMATION FOR SEQ ID NO: 837:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

TTTTTACTGGT ACAGTCTCAA

20

(2) INFORMATION FOR SEQ ID NO: 838:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

TTTACTGGTA CAGTCTCAAT

20

(2) INFORMATION FOR SEQ ID NO: 839:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

TTACTGGTAC AGTCTCAATA

20

(2) INFORMATION FOR SEQ ID NO: 840:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

09784674.03404

TACTGGTACA GTCTCAATAG

20

(2) INFORMATION FOR SEQ ID NO: 841:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

ACTGGTACAG TCTCAATAGG

20

(2) INFORMATION FOR SEQ ID NO: 842:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

CTGGTACAGT CTCAATAGGG

20

(2) INFORMATION FOR SEQ ID NO: 843:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

TGGTACAGTC TCAATAGGGC

20

(2) INFORMATION FOR SEQ ID NO: 844:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

GGTACAGTCT CAATAGGGCT

20

(2) INFORMATION FOR SEQ ID NO: 845:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GTACAGTCTC AATAGGGCTA

20

(2) INFORMATION FOR SEQ ID NO: 846:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

TACAGTCTCA ATAGGGCTAA

20

(2) INFORMATION FOR SEQ ID NO: 847:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

ACAGTCTCAA TAGGGCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 848:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

CAGTCTCAAT AGGGCTAATG

20

(2) INFORMATION FOR SEQ ID NO: 849:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

AGTCTCAATA GGGCTAATGG

20

(2) INFORMATION FOR SEQ ID NO: 850:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GTCTCAATAG GGCTAATGGG

20

(2) INFORMATION FOR SEQ ID NO: 851:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

TCTCAATAGG GCTAATGGGA

20

(2) INFORMATION FOR SEQ ID NO: 852:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

CTCAATAGGG CTAATGGGAA

20

(2) INFORMATION FOR SEQ ID NO: 853:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

TCAATAGGGC TAATGGGAAA

20

(2) INFORMATION FOR SEQ ID NO: 854:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

CAATAGGGCT AATGGGAAAA

20

(2) INFORMATION FOR SEQ ID NO: 855:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

AATAGGGCTA ATGGGAAAAT

20

(2) INFORMATION FOR SEQ ID NO: 856:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

ATAGGGCTAA TGGGAAAATT

20

(2) INFORMATION FOR SEQ ID NO: 857:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

TAGGGCTAAT GGGAAAATTT

20

(2) INFORMATION FOR SEQ ID NO: 858:

09784674.021501
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

AGGGCTAATG GGAAAATTTA

20

(2) INFORMATION FOR SEQ ID NO: 859:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GGGCTAATGG GAAAATTTAA

20

(2) INFORMATION FOR SEQ ID NO: 860:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

GGCTAATGGG AAAATTTAAA

20

(2) INFORMATION FOR SEQ ID NO: 861:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GCTAATGGGA AAATTTAAAG

20

(2) INFORMATION FOR SEQ ID NO: 862:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

CTAATGGGAA AATTTAAAGT

20

(2) INFORMATION FOR SEQ ID NO: 863:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

TAATGGGAAA ATTTAAAGTG

20

(2) INFORMATION FOR SEQ ID NO: 864:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

AATGGGAAAA TTAAAGTGC

20

(2) INFORMATION FOR SEQ ID NO: 865:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

ATGGGAAAAT TTAAAGTGCA

20

(2) INFORMATION FOR SEQ ID NO: 866:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

TGGGAAAATT TAAAGTGCAA

20

(2) INFORMATION FOR SEQ ID NO: 867:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

GGGAAAATTT AAAGTGCAAC

20

(2) INFORMATION FOR SEQ ID NO: 868:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GGAAAATTTA AAGTGCAACC

20

(2) INFORMATION FOR SEQ ID NO: 869:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

GAAAATTTAA AGTGCAACCA

20

(2) INFORMATION FOR SEQ ID NO: 870:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

AAAATTTAAA GTGCAACCAA

20

(2) INFORMATION FOR SEQ ID NO: 871:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

AAATTTAAAG TGCAACCAAT

20

(2) INFORMATION FOR SEQ ID NO: 872:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

AATTTAAAGT GCAACCAATC

20

(2) INFORMATION FOR SEQ ID NO: 873:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

ATTTAAAGTG CAACCAATCT

20

(2) INFORMATION FOR SEQ ID NO: 874:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

TTTAAAGTGC AACCAATCTG

20

(2) INFORMATION FOR SEQ ID NO: 875:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

TTAAAGTGCA ACCAATCTGA

20

(2) INFORMATION FOR SEQ ID NO: 876:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

TAAAGTGCAA CCAATCTGAG

20

(2) INFORMATION FOR SEQ ID NO: 877:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

AAAGTGCAAC CAATCTGAGT

20

(2) INFORMATION FOR SEQ ID NO: 878:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

AAGTGCAACC AATCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO: 879:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

AGTGCAACCA ATCTGAGTCA

20

(2) INFORMATION FOR SEQ ID NO: 880:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GTGCAACCAA TCTGAGTCAA

20

(2) INFORMATION FOR SEQ ID NO: 881:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

TGCAACCAAT CTGAGTCAAC

20

(2) INFORMATION FOR SEQ ID NO: 882:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GCAACCAATC TGAGTCAACA

20

(2) INFORMATION FOR SEQ ID NO: 883:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

CAACCAATCT GAGTCAACAG

20

(2) INFORMATION FOR SEQ ID NO: 884:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

AACCAATCTG AGTCAACAGA

20

(2) INFORMATION FOR SEQ ID NO: 885:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

ACCAATCTGA GTCAACAGAT

20

(2) INFORMATION FOR SEQ ID NO: 886:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

CCAATCTGAG TCAACAGATT

20

(2) INFORMATION FOR SEQ ID NO: 887:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

CAATCTGAGT CAACAGATTT

20

(2) INFORMATION FOR SEQ ID NO: 888:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

AATCTGAGTC AACAGATTTC

20

(2) INFORMATION FOR SEQ ID NO: 889:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

ATCTGAGTCA ACAGATTCT

20

(2) INFORMATION FOR SEQ ID NO: 890:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

TCTGAGTCAA CAGATTCTT

20

(2) INFORMATION FOR SEQ ID NO: 891:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

CTGAGTCAAC AGATTCTTC

20

(2) INFORMATION FOR SEQ ID NO: 892:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10971464-021501

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

TGAGTCAACA GATTTCTTCC

20

(2) INFORMATION FOR SEQ ID NO: 893:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

GAGTCAACAG ATTTCTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 894:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

AGTCAACAGA TTTCTTCCAA

20

(2) INFORMATION FOR SEQ ID NO: 895:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GTCAACAGAT TTCTTCCAAT

20

(2) INFORMATION FOR SEQ ID NO: 896:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

TCAACAGATT TCTTCCAATT

20

(2) INFORMATION FOR SEQ ID NO: 897:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

CAACAGATTT CTTCCAATTA

20

(2) INFORMATION FOR SEQ ID NO: 898:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

AACAGATTTC TTCCAATTAT

20

(2) INFORMATION FOR SEQ ID NO: 899:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

ACAGATTCT TCCAATTATG

20

(2) INFORMATION FOR SEQ ID NO: 900:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

10971464-03450

CAGATTCTT CCAATTATGT

20

(2) INFORMATION FOR SEQ ID NO: 901:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

AGATTCTTC CAATTATGTT

20

(2) INFORMATION FOR SEQ ID NO: 902:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GATTCTTCC AATTATGTTG

20

(2) INFORMATION FOR SEQ ID NO: 903:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

ATTCTTCCA ATTATGTTGA

20

(2) INFORMATION FOR SEQ ID NO: 904:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

TTTCTTCCAA TTATGTTGAC

20

(2) INFORMATION FOR SEQ ID NO: 905:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

TTCTTCCAAT TATGTTGACA

20

(2) INFORMATION FOR SEQ ID NO: 906:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

TCTTCCAATT ATGTTGACAG

20

(2) INFORMATION FOR SEQ ID NO: 907:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

CTTCCAATTA TGTGACAGG

20

(2) INFORMATION FOR SEQ ID NO: 908:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

TTCCAATTAT GTTGACAGGT

20

(2) INFORMATION FOR SEQ ID NO: 909:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

TCCAATTATG TTGACAGGTG

20

(2) INFORMATION FOR SEQ ID NO: 910:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

CCAATTATGT TGACAGGTGT

20

(2) INFORMATION FOR SEQ ID NO: 911:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

CAATTATGTT GACAGGTGTA

20

(2) INFORMATION FOR SEQ ID NO: 912:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

AATTATGTTG ACAGGTGTAG

20

(2) INFORMATION FOR SEQ ID NO: 913:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

ATTATGTTGA CAGGTGTAGG

20

(2) INFORMATION FOR SEQ ID NO: 914:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

TTATGTTGAC AGGTGTAGGT

20

(2) INFORMATION FOR SEQ ID NO: 915:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

TATGTTGACA GGTGTAGGTC

20

(2) INFORMATION FOR SEQ ID NO: 916:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

ATGTTGACAG GTGTAGGTCC

20

(2) INFORMATION FOR SEQ ID NO: 917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

TGTTGACAGG TGTAGGTCCT

20

(2) INFORMATION FOR SEQ ID NO: 918:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

GTTGACAGGT GTAGGTCCTA

20

(2) INFORMATION FOR SEQ ID NO: 919:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

TTGACAGGTG TAGGTCCTAC

20

(2) INFORMATION FOR SEQ ID NO: 920:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

09784674-021501

TGACAGGTGT AGGTCCTACT

20

(2) INFORMATION FOR SEQ ID NO: 921:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GACAGGTGTA GGCCTACTA

20

(2) INFORMATION FOR SEQ ID NO: 922:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

ACAGGTGTAG GTCCTACTAA

20

(2) INFORMATION FOR SEQ ID NO: 923:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

CAGGTGTAGG TCCTACTAAT

20

(2) INFORMATION FOR SEQ ID NO: 924:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

AGGTGTAGGT CCTACTAATA

20

(2) INFORMATION FOR SEQ ID NO: 925:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GGTGTAGGTC CTACTAATAC

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(2) INFORMATION FOR SEQ ID NO: 926:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GTGTAGGTCC TACTAATACT

20

(2) INFORMATION FOR SEQ ID NO: 927:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

TGTAGGTCCT ACTAATACTG

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(2) INFORMATION FOR SEQ ID NO: 928:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

GTAGGTCCTA CTAATACTGT

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(2) INFORMATION FOR SEQ ID NO: 929:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

TAGGTCCTAC TAATACTGTA

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(2) INFORMATION FOR SEQ ID NO: 930:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

AGGTCCTACT AATACTGTAC

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(2) INFORMATION FOR SEQ ID NO: 931:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

GGTCCTACTA ATACTGTACC

20

(2) INFORMATION FOR SEQ ID NO: 932:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

GTCCTACTAA TACTGTACCT

20

(2) INFORMATION FOR SEQ ID NO: 933:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

TCCTACTAAT ACTGTACCTA

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(2) INFORMATION FOR SEQ ID NO: 934:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

CCTACTAATA CTGTACCTAT

20

(2) INFORMATION FOR SEQ ID NO: 935:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

10971464-1031504

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

CTACTAATAC TGTACCTATA

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(2) INFORMATION FOR SEQ ID NO: 936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

TACTAATACT GTACCTATAG

20

(2) INFORMATION FOR SEQ ID NO: 937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

ACTAATACTG TACCTATAGC

20

(2) INFORMATION FOR SEQ ID NO: 938:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

CTAATACTGT ACCTATAGCT

20

(2) INFORMATION FOR SEQ ID NO: 939:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

TAATACTGTA CCTATAGCTT

20

(2) INFORMATION FOR SEQ ID NO: 940:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

09784674 021501
FOIA b7D "4294860

AATACTGTAC CTATAGCTTT

20

(2) INFORMATION FOR SEQ ID NO: 941:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

ATACTGTACC TATAGCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 942:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

TACTGTACCT ATAGCTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 943:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

ACTGTACCTA TAGCTTTATG

20

(2) INFORMATION FOR SEQ ID NO: 944:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

CTGTACCTAT AGCTTTATGT

20

(2) INFORMATION FOR SEQ ID NO: 945:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

TGTACCTATA GCTTTATGTC

20

(2) INFORMATION FOR SEQ ID NO: 946:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GTACCTATAG CTTTATGTCC

20

(2) INFORMATION FOR SEQ ID NO: 947:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

TACCTATAGC TTTATGTCCA

20

(2) INFORMATION FOR SEQ ID NO: 948:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

ACCTATAGCT TTATGTCCAC

20

(2) INFORMATION FOR SEQ ID NO: 949:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10971464-1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

CCTATAGCTT TATGTCCACA

20

(2) INFORMATION FOR SEQ ID NO: 950:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

CTATAGCTTT ATGTCCACAG

20

(2) INFORMATION FOR SEQ ID NO: 951:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

TATAGCTTTA TGTCCACAGA

20

(2) INFORMATION FOR SEQ ID NO: 952:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

ATAGCTTTAT GTCCACAGAT

20

(2) INFORMATION FOR SEQ ID NO: 953:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

TAGCTTTATG TCCACAGATT

20

(2) INFORMATION FOR SEQ ID NO: 954:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

AGCTTTATGT CCACAGATTT

20

(2) INFORMATION FOR SEQ ID NO: 955:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GCTTTATGTC CACAGATTTC

20

(2) INFORMATION FOR SEQ ID NO: 956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

CTTTATGTCC ACAGATTCT

20

(2) INFORMATION FOR SEQ ID NO: 957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

TTTATGTCCA CAGATTCTA

20

(2) INFORMATION FOR SEQ ID NO: 958:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

TTATGTCCAC AGATTCTAT

20

(2) INFORMATION FOR SEQ ID NO: 959:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

TATGTCCACA GATTCTATG

20

(2) INFORMATION FOR SEQ ID NO: 960:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

TTATGTCCAC AGATTCTAT

ATGTCCACAG ATTTCTATGA

20

(2) INFORMATION FOR SEQ ID NO: 961:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

TGTCCACAGA TTTCTATGAG

20

(2) INFORMATION FOR SEQ ID NO: 962:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GTCCACAGAT TTCTATGAGT

20

(2) INFORMATION FOR SEQ ID NO: 963:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

0971464-1021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

TCCACAGATT TCTATGAGTA

20

(2) INFORMATION FOR SEQ ID NO: 964:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

CCACAGATTT CTATGAGTAT

20

(2) INFORMATION FOR SEQ ID NO: 965:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

CACAGATTTT TATGAGTATC

20

(2) INFORMATION FOR SEQ ID NO: 966:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

ACAGATTCT ATGAGTATCT

20

(2) INFORMATION FOR SEQ ID NO: 967:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

CAGATTCTA TGAGTATCTG

20

(2) INFORMATION FOR SEQ ID NO: 968:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

AGATTCTAT GAGTATCTGA

20

(2) INFORMATION FOR SEQ ID NO: 969:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GATTTCTATG AGTATCTGAT

20

(2) INFORMATION FOR SEQ ID NO: 970:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

ATTCTCTATGA GTATCTGATC

20

(2) INFORMATION FOR SEQ ID NO: 971:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

TTTCTATGAG TATCTGATCA

20

(2) INFORMATION FOR SEQ ID NO: 972:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

TTCTATGAGT ATCTGATCAT

20

(2) INFORMATION FOR SEQ ID NO: 973:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

TCTATGAGTA TCTGATCATA

20

(2) INFORMATION FOR SEQ ID NO: 974:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

CTATGAGTAT CTGATCATAC

20

(2) INFORMATION FOR SEQ ID NO: 975:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

TATGAGTATC TGATCATACT

20

(2) INFORMATION FOR SEQ ID NO: 976:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

ATGAGTATCT GATCATACTG

20

(2) INFORMATION FOR SEQ ID NO: 977:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

TGAGTATCTG ATCATACTGT

20

(2) INFORMATION FOR SEQ ID NO: 978:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GAGTATCTGA TCATACTGTC

20

(2) INFORMATION FOR SEQ ID NO: 979:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

AGTATCTGAT CATACTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 980:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

GTATCTGATC ATACTGTCTT

20

(2) INFORMATION FOR SEQ ID NO: 981:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

TATCTGATCA TACTGTCTTA

20

(2) INFORMATION FOR SEQ ID NO: 982:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

ATCTGATCAT ACTGTCTTAC

20

(2) INFORMATION FOR SEQ ID NO: 983:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

TCTGATCATA CTGTCTTACT

20

(2) INFORMATION FOR SEQ ID NO: 984:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

CTGATCATAC TGTCTTACTT

20

(2) INFORMATION FOR SEQ ID NO: 985:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

TGATCATACT GTCTTACTTT

20

(2) INFORMATION FOR SEQ ID NO: 986:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GATCATACTG TCTTACTTTG

20

(2) INFORMATION FOR SEQ ID NO: 987:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

ATCATACTGT CTTACTTTGA

20

(2) INFORMATION FOR SEQ ID NO: 988:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

TCATACTGTC TTACTTTGAT

20

(2) INFORMATION FOR SEQ ID NO: 989:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

CATACTGTCT TACTTTGATA

20

(2) INFORMATION FOR SEQ ID NO: 990:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

ATACTGTCTT ACTTTGATAA

20

(2) INFORMATION FOR SEQ ID NO: 991:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

TACTGTCTTA CTTTGATAAA

20

(2) INFORMATION FOR SEQ ID NO: 992:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

ACTGTCTTAC TTTGATAAAA

20

(2) INFORMATION FOR SEQ ID NO: 993:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

CTGTCTTACT TTGATAAAAC

20

(2) INFORMATION FOR SEQ ID NO: 994:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

TGTCTTACTT TGATAAAACC

20

(2) INFORMATION FOR SEQ ID NO: 995:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

GTCTTACTTT GATAAAACCT

20

(2) INFORMATION FOR SEQ ID NO: 996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

TCTTACTTTG ATAAACCTC

20

(2) INFORMATION FOR SEQ ID NO: 997:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

CTTACTTTGA TAAACCTCC

20

(2) INFORMATION FOR SEQ ID NO: 998:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

TTACTTTGAT AAAACCTCCA

20

(2) INFORMATION FOR SEQ ID NO: 999:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

TACTTTGATA AAACCTCCAA

20

(2) INFORMATION FOR SEQ ID NO: 1000:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

ACTTTGATAA AACCTCCAAT

20

(2) INFORMATION FOR SEQ ID NO: 1001:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

CTTTGATAAA ACCTCCAATT

20

(2) INFORMATION FOR SEQ ID NO: 1002:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

TTTGATAAAA CCTCCAATTC

20

(2) INFORMATION FOR SEQ ID NO: 1003:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

TTGATAAAAC CTCCAATTCC

20

(2) INFORMATION FOR SEQ ID NO: 1004:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

TGATAAAACC TCCAATTCCC

20

(2) INFORMATION FOR SEQ ID NO: 1005:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

GATAAAACCT CCAATTCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1006:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

ATAAAACCTC CAATCCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

TAAACCTCC AATCCCCCT

20

(2) INFORMATION FOR SEQ ID NO: 1008:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

AAACCTCCA ATTCCCCCTA

20

(2) INFORMATION FOR SEQ ID NO: 1009:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

AAACCTCCAA TTCCCCCTAT

20

(2) INFORMATION FOR SEQ ID NO: 1010:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

AACCTCCAAT TCCCCCTATC

20

(2) INFORMATION FOR SEQ ID NO: 1011:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

ACCTCCAATT CCCCCTATCA

20

(2) INFORMATION FOR SEQ ID NO: 1012:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

CCTCCAATTC CCCCTATCAT

20

(2) INFORMATION FOR SEQ ID NO: 1013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

CTCCAATTCC CCCTATCATT

20

(2) INFORMATION FOR SEQ ID NO: 1014:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

TCCAATTCCC CCTATCATTT

20

(2) INFORMATION FOR SEQ ID NO: 1015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

0971464-03450

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

CCAATTCCCC CTATCATTTT

20

(2) INFORMATION FOR SEQ ID NO: 1016:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

CAATTCCCC TATCATTTTT

20

(2) INFORMATION FOR SEQ ID NO: 1017:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

AATCCCCCT ATCATTTTTG

20

(2) INFORMATION FOR SEQ ID NO: 1018:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

ATTCCCCCTA TCATTTTGG

20

(2) INFORMATION FOR SEQ ID NO: 1019:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

TTCCCCCTAT CATTTTGGT

20

(2) INFORMATION FOR SEQ ID NO: 1020:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

TCCCCCTATC ATTTTGGTT

20

(2) INFORMATION FOR SEQ ID NO: 1021:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

CCCCCTATCA TTTTGGTTT

20

(2) INFORMATION FOR SEQ ID NO: 1022:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

CCCCTATCAT TTTGGTTTC

20

(2) INFORMATION FOR SEQ ID NO: 1023:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

CCCTATCATT TTTGGTTTCC

20

(2) INFORMATION FOR SEQ ID NO: 1024:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

CCTATCATTT TTGGTTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 1025:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

CTATCATTTT TGGTTTCCAT

20

(2) INFORMATION FOR SEQ ID NO: 1026:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

TATCATTTTT GGTTCATC

20

(2) INFORMATION FOR SEQ ID NO: 1027:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

ATCATTTTTG GTTCCATCT

20

(2) INFORMATION FOR SEQ ID NO: 1028:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

TCATTTTTGG TTTCCATCTT

20

(2) INFORMATION FOR SEQ ID NO: 1029:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

CATTTTGGT TTCCATCTTC

20

(2) INFORMATION FOR SEQ ID NO: 1030:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

ATTTTGGTT TCCATCTTCC

20

(2) INFORMATION FOR SEQ ID NO: 1031:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

TTTTTGGTTT CCATCTTCCT

20

(2) INFORMATION FOR SEQ ID NO: 1032:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

TTTTGGTTTC CATCTTCCTG

20

(2) INFORMATION FOR SEQ ID NO: 1033:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

TTTGGTTTCC ATCTTCCTGG

20

(2) INFORMATION FOR SEQ ID NO: 1034:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

TTGGTTTCCA TCTTCCTGGC

20

(2) INFORMATION FOR SEQ ID NO: 1035:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

TGGTTTCCAT CTCCTGGCA

20

(2) INFORMATION FOR SEQ ID NO: 1036:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

GGTTTCCATC TTCCTGGCAA

20

(2) INFORMATION FOR SEQ ID NO: 1037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

GTTTCCATCT TCCTGGCAAA

20

(2) INFORMATION FOR SEQ ID NO: 1038:

0971464-103501

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

TTTCCATCTT CCTGGCAAAC

20

(2) INFORMATION FOR SEQ ID NO: 1039:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

TTCCATCTTC CTGGCAAAC

20

(2) INFORMATION FOR SEQ ID NO: 1040:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

TTCCATCTTC CTGGCAAAC

TCCATCTTCC TGGCAAACCTC

20

(2) INFORMATION FOR SEQ ID NO: 1041:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

CCATCTTCCT GGCAAACCTCA

20

(2) INFORMATION FOR SEQ ID NO: 1042:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

CATCTTCCTG GCAAACCTCAT

20

(2) INFORMATION FOR SEQ ID NO: 1043:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

ATCTTCCTGG CAAACTCATT

20

(2) INFORMATION FOR SEQ ID NO: 1044:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

TCTTCCTGGC AAACATCATTT

20

(2) INFORMATION FOR SEQ ID NO: 1045:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

CTTCCTGGCA AAACATTTTC

20

(2) INFORMATION FOR SEQ ID NO: 1046:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

TTCCTGGCAA ACTCATTTCT

20

(2) INFORMATION FOR SEQ ID NO: 1047:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

TCCTGGCAAA CTCATTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 1048:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

CCTGGCAAAC TCATTTCTTC

20

(2) INFORMATION FOR SEQ ID NO: 1049:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

CTGGCAAACCT CATTCTTTCT

20

(2) INFORMATION FOR SEQ ID NO: 1050:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

TGGCAAACCTC ATTTCTTCTA

20

(2) INFORMATION FOR SEQ ID NO: 1051:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

GGCAAACCTCA TTTCTTCTAA

20

(2) INFORMATION FOR SEQ ID NO: 1052:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

GCAAATCAT TTCTTCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 1053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

CAAATCATT TCTTCTAATA

20

(2) INFORMATION FOR SEQ ID NO: 1054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

AAATCATT CTTCTAATAC

20

(2) INFORMATION FOR SEQ ID NO: 1055:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

AAATCATTTC TTCTAATACT

20

(2) INFORMATION FOR SEQ ID NO: 1056:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

ACTCATTCTCT TCTAATACTG

20

(2) INFORMATION FOR SEQ ID NO: 1057:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

CTCATTCTCTT CTAATACTGT

20

(2) INFORMATION FOR SEQ ID NO: 1058:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

TCATTTCTTC TAATACTGTA

20

(2) INFORMATION FOR SEQ ID NO: 1059:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

CATTTCTTCT AATACTGTAT

20

(2) INFORMATION FOR SEQ ID NO: 1060:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

105720-1298/60

ATTCTTCTA ATACTGTATC

20

(2) INFORMATION FOR SEQ ID NO: 1061:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

TTTCTTCTAA TACTGTATCA

20

(2) INFORMATION FOR SEQ ID NO: 1062:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

TTCTTCTAAT ACTGTATCAT

20

(2) INFORMATION FOR SEQ ID NO: 1063:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

TCTTCTAATA CTGTATCATC

20

(2) INFORMATION FOR SEQ ID NO: 1064:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

CTTCTAATAC TGTATCATCT

20

(2) INFORMATION FOR SEQ ID NO: 1065:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

TTCTAATACT GTATCATCTG

20

(2) INFORMATION FOR SEQ ID NO: 1066:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

TCTAATACTG TATCATCTGC

20

(2) INFORMATION FOR SEQ ID NO: 1067:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

CTAATACTGT ATCATCTGCT

20

(2) INFORMATION FOR SEQ ID NO: 1068:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

TAATACTGTA TCATCTGCTC

20

(2) INFORMATION FOR SEQ ID NO: 1069:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

AATACTGTAT CATCTGCTCC

20

(2) INFORMATION FOR SEQ ID NO: 1070:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

ATACTGTATC ATCTGCTCCT

20

(2) INFORMATION FOR SEQ ID NO: 1071:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

TACTGTATCA TCTGCTCCTG

20

(2) INFORMATION FOR SEQ ID NO: 1072:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

ACTGTATCAT CTGCTCCTGT

20

(2) INFORMATION FOR SEQ ID NO: 1073:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

CTGTATCATC TGCTCCTGTA

20

(2) INFORMATION FOR SEQ ID NO: 1074:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

TGTATCATCT GCTCCTGTAT

20

(2) INFORMATION FOR SEQ ID NO: 1075:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

GTATCATCTG CTCCTGTATC

20

(2) INFORMATION FOR SEQ ID NO: 1076:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

TATCATCTGC TCCTGTATCT

20

(2) INFORMATION FOR SEQ ID NO: 1077:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

ATCATCTGCT CCTGTATCTA

20

(2) INFORMATION FOR SEQ ID NO: 1078:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

TCATCTGCTC CTGTATCTAA

20

(2) INFORMATION FOR SEQ ID NO: 1079:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

CATCTGCTCC TGTATCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 1080:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

05734674.021501
T05F20.424B250

ATCTGCTCCT GTATCTAATA

20

(2) INFORMATION FOR SEQ ID NO: 1081:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

TCTGCTCCTG TATCTAATAG

20

(2) INFORMATION FOR SEQ ID NO: 1082:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

CTGCTCCTGT ATCTAATAGA

20

(2) INFORMATION FOR SEQ ID NO: 1083:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

TGCTCCTGTA TCTAATAGAG

20

(2) INFORMATION FOR SEQ ID NO: 1084:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

GCTCCTGTAT CTAATAGAGC

20

(2) INFORMATION FOR SEQ ID NO: 1085:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

CTCCTGTATC TAATAGAGCT

20

(2) INFORMATION FOR SEQ ID NO: 1086:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

0971464-1021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

TCCTGTATCT AATAGAGCTT

20

(2) INFORMATION FOR SEQ ID NO: 1087:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

CCTGTATCTA ATAGAGCTTC

20

(2) INFORMATION FOR SEQ ID NO: 1088:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

CTGTATCTAA TAGAGCTTCC

20

(2) INFORMATION FOR SEQ ID NO: 1089:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

TGTATCTAAT AGAGCTTCCT

20

(2) INFORMATION FOR SEQ ID NO: 1090:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GTATCTAATA GAGCTTCCTT

20

(2) INFORMATION FOR SEQ ID NO: 1091:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

TATCTAATAG AGCTTCCTTT

20

(2) INFORMATION FOR SEQ ID NO: 1092:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

ATCTAATAGA GCTTCCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 1093:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

TCTAATAGAG CTTCTTTAG

20

(2) INFORMATION FOR SEQ ID NO: 1094:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

CTAATAGAGC TTCCTTTAGT

20

(2) INFORMATION FOR SEQ ID NO: 1095:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

09784674-021501

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

TAATAGAGCT TCCTTTAGTT

20

(2) INFORMATION FOR SEQ ID NO: 1096:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

AATAGAGCTT CCTTTAGTTG

20

(2) INFORMATION FOR SEQ ID NO: 1097:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

ATAGAGCTTC CTTTAGTTGC

20

(2) INFORMATION FOR SEQ ID NO: 1098:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

TAGAGCTTCC TTTAGTTGCC

20

(2) INFORMATION FOR SEQ ID NO: 1099:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

AGAGCTTCCT TTAGTTGCCC

20

(2) INFORMATION FOR SEQ ID NO: 1100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

GAGCTTCCTT TAGTTGCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

AGCTTCCTTT AGTTGCCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GCTTCCTTTA GTTGCCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

CTTCCTTTAG TTGCCCCCCT

20

(2) INFORMATION FOR SEQ ID NO: 1104:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

TTCCTTTAGT TGCCCCCCTA

20

(2) INFORMATION FOR SEQ ID NO: 1105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

TCCTTTAGTT GCCCCCCTAT

20

(2) INFORMATION FOR SEQ ID NO: 1106:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

CCTTTAGTTG CCCCCCTATC

20

(2) INFORMATION FOR SEQ ID NO: 1107:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

CTTTAGTTGC CCCCCTATCT

20

(2) INFORMATION FOR SEQ ID NO: 1108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

TTTAGTTGCC CCCCTATCTT

20

(2) INFORMATION FOR SEQ ID NO: 1109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

TTAGTTGCCC CCCTATCTTT

20

(2) INFORMATION FOR SEQ ID NO: 1110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

TAGTTGCCCC CCTATCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 1111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

AGTTGCCCCC CTATCTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 1112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GTTGCCCCC TATCTTTATT

20

(2) INFORMATION FOR SEQ ID NO: 1113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

TTGCCCCCCT ATCTTTATTG

20

(2) INFORMATION FOR SEQ ID NO: 1114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

TGCCCCCCTA TCTTTATTGT

20

(2) INFORMATION FOR SEQ ID NO: 1115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GCCCCCTAT CTTTATTGTG

20

(2) INFORMATION FOR SEQ ID NO: 1116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

CCCCCCTATC TTTATTGTGA

20

(2) INFORMATION FOR SEQ ID NO: 1117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

CCCCCTATCT TTATTGTGAC

20

(2) INFORMATION FOR SEQ ID NO: 1118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

CCCCTATCTT TATTGTGACG

20

(2) INFORMATION FOR SEQ ID NO: 1119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

CCCTATCTTT ATTGTGACGA

20

(2) INFORMATION FOR SEQ ID NO: 1120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

CCTATCTTTA TTGTGACGAG

20

(2) INFORMATION FOR SEQ ID NO: 1121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

CTATCTTTAT TGTGACGAGG

20

(2) INFORMATION FOR SEQ ID NO: 1122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

TATCTTTATT GTGACGAGGG

20

(2) INFORMATION FOR SEQ ID NO: 1123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

ATCTTTATTG TGACGAGGGG

20

(2) INFORMATION FOR SEQ ID NO: 1124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

TCTTTATTGT GACGAGGGGT

20

(2) INFORMATION FOR SEQ ID NO: 1125:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

CTTTATTGTG ACGAGGGGTC

20

(2) INFORMATION FOR SEQ ID NO: 1126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

TTTATTGTGA CGAGGGGTCG

20

(2) INFORMATION FOR SEQ ID NO: 1127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

TTATTGTGAC GAGGGGTCGT

20

(2) INFORMATION FOR SEQ ID NO: 1128:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

TATTGTGACG AGGGGTCGTT

20

(2) INFORMATION FOR SEQ ID NO: 1129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

ATTGTGACGA GGGGTCGTTG

20

(2) INFORMATION FOR SEQ ID NO: 1130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

TTGTGACGAG GGGTCGTTGC

20

(2) INFORMATION FOR SEQ ID NO: 1131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

TGTGACGAGG GGTCGTTGCC

20

(2) INFORMATION FOR SEQ ID NO: 1132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GTGACGAGGG GTCGTTGCCA

20

(2) INFORMATION FOR SEQ ID NO: 1133:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

TGACGAGGGG TCGTTGCCAA

20

(2) INFORMATION FOR SEQ ID NO: 1134:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GACGAGGGGT CGTTGCCAAA

20

(2) INFORMATION FOR SEQ ID NO: 1135:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

ACGAGGGGTC GTTGCCAAAG

20

(2) INFORMATION FOR SEQ ID NO: 1136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

CGAGGGGTCG TTGCCAAAGA

20

(2) INFORMATION FOR SEQ ID NO: 1137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

GAGGGGTCGT TGCCAAAGAG

20

(2) INFORMATION FOR SEQ ID NO: 1138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

AGGGGTCGTT GCCAAAGAGT

20

(2) INFORMATION FOR SEQ ID NO: 1139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GGGGTCGTTG CCAAAGAGTG

20

(2) INFORMATION FOR SEQ ID NO: 1140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

GGGTCGTTGC CAAAGAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 1141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GGTCGTTGCC AAAGAGTGAT

20

(2) INFORMATION FOR SEQ ID NO: 1142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GTCGTTGCCA AAGAGTGATC

20

(2) INFORMATION FOR SEQ ID NO: 1143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

TCGTTGCCAA AGAGTGATCT

20

(2) INFORMATION FOR SEQ ID NO: 1144:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

CGTTGCCAAA GAGTGATCTG

20

(2) INFORMATION FOR SEQ ID NO: 1145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

GTTGCCAAAG AGTGATCTGA

20

(2) INFORMATION FOR SEQ ID NO: 1146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

TTGCCAAAGA GTGATCTGAG

20

(2) INFORMATION FOR SEQ ID NO: 1147:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

TGCCAAAGAG TGATCTGAGG

20

(2) INFORMATION FOR SEQ ID NO: 1148:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GCCAAAGAGT GATCTGAGGG

20

(2) INFORMATION FOR SEQ ID NO: 1149:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

CCAAAGAGTG ATCTGAGGGA

20

(2) INFORMATION FOR SEQ ID NO: 1150:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

CAAAGAGTGA TCTGAGGGAA

20

(2) INFORMATION FOR SEQ ID NO: 1151:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

AAAGAGTGAT CTGAGGGAAG

20

(2) INFORMATION FOR SEQ ID NO: 1152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

AAGAGTGATC TGAGGGAAGT

20

(2) INFORMATION FOR SEQ ID NO: 1153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

AGAGTGATCT GAGGGAAGTT

20

(2) INFORMATION FOR SEQ ID NO: 1154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

GAGTGATCTG AGGGAAGTTA

20

(2) INFORMATION FOR SEQ ID NO: 1155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

AGTGATCTGA GGAAGTTAA

20

(2) INFORMATION FOR SEQ ID NO: 1156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

GTGATCTGAG GGAAGTTAAA

20

(2) INFORMATION FOR SEQ ID NO: 1157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

TGATCTGAGG GAAGTTAAAG

20

(2) INFORMATION FOR SEQ ID NO: 1158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

GATCTGAGGG AAGTTAAAGG

20

(2) INFORMATION FOR SEQ ID NO: 1159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

ATCTGAGGGA AGTTAAAGGA

20

(2) INFORMATION FOR SEQ ID NO: 1160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

0971464-1 02/20/20

TCTGAGGGAA GTTAAAGGAT

20

(2) INFORMATION FOR SEQ ID NO: 1161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

CTGAGGGAAG TTAAAGGATA

20

(2) INFORMATION FOR SEQ ID NO: 1162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

TGAGGGAAGT TAAAGGATAC

20

(2) INFORMATION FOR SEQ ID NO: 1163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GAGGGAAGTT AAAGGATACA

20

(2) INFORMATION FOR SEQ ID NO: 1164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

AGGGAAGTTA AAGGATACAG

20

(2) INFORMATION FOR SEQ ID NO: 1165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

GGGAAGTTAA AGGATACAGT

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